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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
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seq length: 2000000000
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Copyright (c) 1993 - 2005 Compugen Ltd.
/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11	10	9	8	7	σ	ហ	4	w	2	r	Result No.
198	201.2	271.6	296.2	296.2	326.8	362.4	362.4	2326.4	2674	2674	Score
7.4	7.5	10.2	11.1	11.1	12.2	13.6	13.6	87.0	100.0	100.0	Query
		1779									Query Match Length DB
18	15	17	15	ø	10	17	13	16	17	13	BB
US-10-384-339C-1	US-10-101-510-525	US-10-280-576-19	US-10-121-925-5	US-09-948-802-5	US-09-918-995-1503	7 US-10-660-763-3	US-10-003-295-3	US-10-240-965-256	US-10-660-763-1	US-10-003-295-1	ID
Sequence 1, Appli	Sequence 525, App	Sequence 19, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 1503, Ap	Sequence 3, Appli	Sequence 3, Appli	Sequence 256, App	Sequence 1, Appli	Sequence 1, Appli	Description

45																	28												16	15	14	13	•
170.4	170.4	170.4	170.4	174.6	٠	174.6	•		٠	174.6	174.6	174.6	•	•		•	185.4	185.4						•	•	185.4	185.4	185.4	198	198	9	198	1
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19	18	18	18	16	14	18	17	14	17	17	15	ω	16	18	18	17	19	19	18	18	17	17	17	17	16	15	10	18	18	18	16	16	
US-10-497-641-1	-10-887-	-10-	-10-476-	0-325-4	US-10-161-803-52	-10-620-052A	US-10-291-808-13	0-161-803-5	US-10-305-720-1483	US-10-464-805-2	US-10-292-524-1	US-08-987-689A-1	US-10-325-430-8	-10	-10-	-10-280-576-	-10-897-711-	-10-616-403-	-10-473-9	-10 - 648	-10-287-226-	-10-342-887-103	-10-172-118-	-10-366	-10-269-909-1	US-10-007-926A-222	-09-921-406C-	-10-384	US-10-473-974-219	US-10-776-827-82	US-10-210-120-19	US-10-354-358-101	** * * * * * * * * * * * * * * * * * * *
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ALIGNMENTS

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; TYPE: DNA; ORGANISM: Homo sapiens US-10-003-295-1
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US-10-003-295-1
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1183DIV
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10003295 Publication No. US20020168741A1 GENERAL INFORMATION:
                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 2674; Conservative 0;
121 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGC
                                                                61
                                                                                                    61 GGAACAGCACTATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGC 120
                                                                                                                                                                         1 TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCCGAGGCCGTCCCCAGGAGCAGCTGCCCGTGC
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GCAGGAGTTGCTGCJ SCAGGAGTTGCTGCJ	GCAAGAAGCACTGC! GCAAGAAGCACTGC!	TGAAGAGGAGAACA(TGAAGAGGAGAACA(CACCGAGATGGTGT] CACCGAGATGGTGTT	GCTGACTGTGGAGAO	CGATGAGTCACTGCT 	GTACCAAGGCTTCCT	GGTGGTGGCCATTC <i>I</i> 	FTGCATCCTGAAGG/ TGCATCCTGAAGG/	CCACCAGCTCCTGCT	IGCTCACCACAACCC	GAAAGACAAGGACCC	CCAGTACCGAGCTCT	3CAGCAGCTGCAGC 3CAGCAGCTGCAGC	CAAGCTGAGCCTGCT	TGAGGGCCTGAGCCC TGAGGGCCTGAGCCC	CCGGGCCATCAGCCC	IGACAGGGAGTATGO
TGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCC	GGCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCCAGGCCAAG	CGGAATGAAGAGGAGAACACCCACCCCCGGGAGCGGTGCAGCTGCTGGG	CACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGC	:crgactgrgagagagcgrgcagcacacgcrgaccr 	CGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGA 	CCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTC	TGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCGCA'	AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATT; 	CACCAGCTCCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTG(ggaagctctttgctcaccacaaccgctatgtgctgggcggggctgcgcagctacac 	AGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCA 	GTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGC 	TGGCAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGA	GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGA	CCAAACTGAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAG	GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG	GGGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTG
ACCTGGGCCCCGGCC ACCTGGGCCCCGGCC	CGCTGTGCAGCCAGG GCTGTGCAGCCAGG	gggigcagctgctgc gggigcagctgctgc	TGGTTACGCAGCTGO	TGACCTCAGTGACAC TGACCTCAGTGACAC	CGCTGGAGCCTGGGC CGCTGGAGCCTGGGC	CCGCACCTGACGTCC	CAGCTGCTGCCCGCF 	ACCTGGAGATTAGCA(ggrcactgcaggacc ggrcactgcaggacc	recegecrececaec	acaagtatgtgcgca acaagtatgtgcgca	CCCAAGCCAAGCGCA 	CCCACAGCCAGGACA	AGCAGCTTCGCAAG <i>P</i> AGCAGCTTCGCAAG <i>P</i>	ACGCAGAGGATCTGA ACGCAGAGGATCTGA	GTCAGTCCTGGGCTC STCAGTCCTGGGCTC	ACATGTCCCTGCAGG
3AGCCCC 1260 3AGCCCC 1260	GCCAAGC 1200 CCAAGC 1200		AACAGG 10 AACAGG 10	AGATGAGC 1020 AGATGAGC 1020	BAGCTCC 960	CACCCT. 9	ATCCAGC 840	AGCCIGG 780 AGCCIGG 780	CTGCACG 720	ი—ი	AGCCIGT 600	AAGTACC 540	ATTGAGA 480 ATTGAGA 480	ACCTACA 420 ACCTACA 420	AACTCAG 360 AACTCAG 360	3AGATCA 300 3AGATCA 300	3ACAGTG 240 3ACAGTG 240
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ACCAGGAGCTGCAGAGCATCO	CAGGCTCATGGAGCAGTGCTGGG	GAGTTTGTGGAGAAGGGGGGCC	TGGGAGACCTTCAGCCTGGGGG	GCCCTTAACTACGGCCGCTACT	GGGGTCTATGCAGCCTCAGGGG	3GTGACAGAGAAGAATGTCCTGA 	CATGGAGTACCTGGAGAGCAAGT CATGGAGTACCTGGAGAGCAAGT	GAGGGGGCCCGCCTGCGGTGA	AGCCCATCTACATCGTCATGGAGC	TCCTGAAGCAGTACAGCCACCCCA	AGTCTTGTCGAGAGACGCTCCCAC	;ggaactttggcgaagtgttcagcg ;ggaactttggcgaagtgttcagcg	CCCAAGGACAAGTGGGTGCTGAACC CCCAAGGACAAGTGGGTGCTGAACC	TACTGAGCACCCAGCAGCCCCTCA	CGAACCTGTACCGACTGGAAGGGGT	GALACCEACGCTGGAGATCCTTA	GCTCCTGCAGGATGACCGCCACT
ALLANGARGCTIGLAGAGCATCCGAAAGCGGCATICG 		SAGTITGTGGAGAAGGGGGCCGTCTGCCCTGCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCTGCCCTGCCCTGCCCCCTGCCCCTGCCCCTGCCCCCTGCCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCCTGCCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCTGCCCCCTGCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTCCT	TGGAAACCTTCAGCCTGGGGGCCTCCCCCTATCC 	SCCCTTAACTACGECGCCGCTACTCCTCCGAAAGCGA 	reaggtctatgckecctckegegegctckegackagt 	GTGACAGAGAAGAATGTCCTGAAGATCAGTGACTT GTGACAGAGAAGAATGTCCTGAAGATCAGTGACTT	CATGGAGTACCTGGAGAGCAGCTGCTGCATCCACCG 		AGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGG 	TCTGAAGCAGTACAGCCACCCAACATCGTGCGTCT	WGTCTTGTCGAAGAACGCTCCCACCTGACCTCAAGGC 	;ggaactttggcgaagtgttcagcggacgcctgcgagc 	CCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGT 	TACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTACTACTAACCAAGAAGAGTGGTACCAAGCACCAAGAAGAGTGGTACCAAGAAGAAGAGTGG	CHARC CIGIAC CORC I GERNOGGERANGEC I I I CLIAG 		GCTCCTGCAGGATGACCGCCACTCCACGTCGTCCTC
TCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCTGGGACCTCGAAAGCGGCATCGGTGAGGCTGGGACCTCGAGAGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCTCGGAAAGCATCCGAAAGCATCAGATGAGCATCAGAACCATCAGAAAGCAATCAGAAAGCAAAAAAAA	ATTRICTORY TO A CONTROL OF THE CONTR	AGCAGACACGGGAGTTTGTGGAGAAAGGGGGGCCGTCTGCCCTGCCCTGCCAAGCTGTGTCCTG	GCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCTATCCCAACCTCAGCAATC [CCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTG	AGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGA 	GGAACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAG 	CAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCT	TCCTCCGCACGGAGGGGCCCCCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGATG	CCARAAGCAGCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGG	AAGCGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCA 	TGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGG 	TTGGACGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGACCCGACAACACCCTGG 	GGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGA 	TCGACCACCTACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACA TCGACCACCTACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACA	CCAAGIIC LUGAACCIGIACUGAC I GGAAGGGGAAGGCII ICCIACGAIIC IIICII CAAGIIC CAAGIIC CAAGAIIC CAAGAIC CAAGAACCAAGAACCAAGAAGAAGAAGAAGAAGAAAGA	######################################	CGCCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGCAGGAGCGAG

RESULT 2 US-10-660-763-1 US-10-660-763-1 Sequence 1, Application US/10660763 Publication No. US/20040053130A1 FOR PROTEINS, NUCLEIC FITTLE OF INVENTION: ACID MCLECULES ENCODING HUWAN KINASE PROTEINS, AND USES FILE REFERENCE: CL001189DIVII CURRENT FILING DATE: 2003-09-12 NUMBER OF SEQ 1D NO: 4 SOFTWARE: FRESED for Windows Version 4.0 LENGTH: 367-4 TYPE: DNA 7 TYPE: DN	2641 2641 2641	Qy 2521 AACAATAAAACCACTTGTGCCCACTGAAAAAAAAAAAAA	Qy 2461 ATGCAGCGCGTGTCCTCTGTGTCCCTGCTGCCAGGGCTTCCTCTTCCGGGCAGA 2520	Qy 2341 CCCTTCTCAAGCTGGTGGCCTCTGCAGGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCA 2400
8	D Q 5	P & B &	Qу	B & B &
721 AGARATGCTTGCATCCTTGAAGAAATTCCTTGCAGAATTACCTTGGAATTAGCAGCTTGG 1	ACCAGCACCACCACCAGCTCCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACG	541 AGGAGGCCAGCAAAGACAAGGACCGTGACAAAGGCAAAGGACAAGTATGTGCGCAGCCTGT 600 541 AGGAGGCCAGCAAAGACAAGGACCGTGACAAAGGCCAAAGGACAAGTATGTGCGCAGCCTGT 600 541 AGGAGGCCAGCAAAGACAAAGGACCGTGACAAAGGCCAAAGGACAAAGTATGTGCGCAGCCTACACC 660 601 GGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAACTACACC 660 601 GGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGCGCGTGCGGCTGCGCAACTACACC 660	481 AGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGCGCAAGTACC 540	361 GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGCAGCAGCTTCGCAAGACCTACA 420

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ATGCAGCGCCGTGTCCTCTGTGTCCCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGA
                                                                                  ATGCAGCGCCGTGTCCTCTCTGTGTCCCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGA
                                                                                                                                         TATGCTGACAGCTCTTCACAGTCCTGGACTCCTGCCACCAGCATCCACACTGCCGGCAGG
                                                                                                                                                               TATGCTGACAGCTCTTCACAGTCCTGGACTCCTGCCACCAGCATCCACACTGCCGGCAGG
                                                                                                                                                                                                                    CCCTTCTCAAGCTGGCCTCTGCAGGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCA
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Sequence 256, Application US/10240965

Publication No. US20030165924A1

GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SHIFFMAN, Dov
APPLICANT: SHIFFMAN, Dov
APPLICANT: LAWN, Richard M.
APPLICANT: LAWN, Richard M.
APPLICANT: SEILHAMER, Jeffrey J.
APPLICANT: MIKITA, Thomas
APPLICANT: TAI, Julie
FILE REFERENCE: PA-0025 PCT
CURRENT APPLICATION NUMBER: US/10/240,965

CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 00/195,106
PRIOR APPLICATION DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 276
SOFTWARE: PERL PROGram
SEQ ID NO 256
LENGTH: 2889
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; OTHER INFORMATION: Incyte ID No. US20030165924A1 997347.6
US-10-240-965-256
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Best Local Similarity
Matches 2558; Conservat
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                                                    CAGCCAAACTGA-GGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAG
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Pred. No. 0;
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2371 TAGGTGCAGCTCCTCAGCGGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCCTGGACT 2430	CABCTISTISM TACACISSISCATIC CCISASSISCASSISSISCASCISCISCACT 1817	Ov 1392
38 TCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCAGGCC		1392
11 TCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCAGGCC	CCAAGTTCTCGCTCCCTCCACCGCTGCAGCTCATTCCGGAGGTGCAGAAGCCCCTGCATG 1557	1498
251 995CLR1949CL1995CR9COSCCA9511CASCACCATCLASCACSACTICASCAGGACTICAGACTICACACTICAGACTICAGACTICAGACTICAGACTICAGACTICAGACTICAGACTICAGACTICACACTICAGACT	G1391	Qy 1381 CCAAGTTCTCG
18 GCCGTCTGCCCTGCCCAAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCT	97	1438
2191 GCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGCAGCAGCAGTGCT 2250		1321
58 GGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAAGGGGG	CGCCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCGTCGTCGTGGAGCAGGAGCAGG 1320	Qy , 1261 CGCCTGTC
	TGCAGGCCCAGCAGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCC 1377	Db 1318 TGCAGGCC
2071 ACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGGGAGAGACCTTCAGCCTGG 2130	1260	_
	GGCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCCAGGCCAAGC 1200	Qy 1141 GGCAAGTC
22/8 IGHANGHICHGIGHCIIIGGGHIGICCCCGTGAAGTGGACCTGAGGCCCTTAACTACGGCCGCT 2070	AGCTCCGGAATGAAGAGGAGAACACCCACCCCGGGAGCGGGTGCAGCTGCTGGGCAAGA 1257	Db 1198 AGCTCCGC
51 TGAAGATCAGTGACTTTGGGATGATCCCGAGAGGAAGCCGATTGGGGTCTATGCAGCCTCAG	1140	1
18 AGTGCTGCATCCACCGGGACCTGGCTGGGAACTGCCTGGTGACAGAAGAATGTCC	TGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGG 1080	Db 1138 TGGCTGTC
1891 AGTGCTGCATCCACCGGGACCTGGCTGGTCGGAACTGCCTGGTGACAGAGAAGAATGTCC 1950	1137	1078
2158 TGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCATGCAGTACCTGGAGAGCA 2217	AGCTGAACGAGCTGACTGTGGAGAGCGCAGCACACGCTGACCTCAGTGACAGATGAGC 1020 CD	961
2098 AGCTTGTGCAGGGGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGGGCCCGCCTGCGGG 2157	GTGTCACGTTCGATGACTCACTGCGAGGGAGGGTGAACCCCTGGAGCCTGGGAGCTCC 1077	Db 1018 GTGTCACC
71 AGCTTGTGCAGGGGGGGCGACTTCCTGACCTTCCTCCGCACGGACGG	960	901 G
38 CCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGG	TGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGAAGGTCCCACCCT 900	Qy 841 CTGAGGCT
1711 CCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGG 1770	10	898 T
1931 CHCCLUMCELCANGECEANGELLECHAGE LACACGAMERA CELIGRAGEAGEACHACE 1/10 1978 CACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACC 2037	TGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGCTGCCAGCTGCTGCCCGCATCCAGC 840	781
18 GEGGACGCCTGCGAGCCGAACACCCTGGTGGCTGTTTTTTTT		838
1591 GCGGACGCCTGCGAGCCGACACACCCCTGGTGGCGGTGAAGTCTTGTCGAGAGACACCTCC 1650	TTTCCATCCTTGAACGATACCTGCAAGATCACGAAGATCACCTGCAAGATCACCTGCCTG	Ov 721 AGGAGATO
1858 ACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCGAAGTGTTCA 1917	CACCACCAGCTCCTGCTGCCGGCCTGCGGGTCACTGCAGGACCTGCACG 720	661
1798 TCACCAAGAAGACTGGTGTTGTCCTGCACAAGGGCTGTGCCCAAGGACAAGTGGGTGCTGA 1857	7	718 GGAAG
1471 TCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCCCAAGGACAAGTGGGTGCTGA 1530		601 GGAAG
38 GGGAAGGCTTTCCTAGCATTCCTTTGCTCATCGACCACCTACTGAGCACCCAGCAGCCCC	AGGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCAAGGACAAGTITTTTTTTTTT	Qy 541 AGGAGGCC
1678 GGGATGGTCTGCCCCGGCACTTCATCATCCAGTCCTTGGATAACCTGTACCGACTGGAAG 1737	AGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGTACC 657	Db 598 AGCTGAAG
92	540	81
18 CTGGGGACTTCCTGGTGCGGGAGAGCCAGGGCAAGCAGGAGTACGTGCTGTCGGTGCTGT	CGAGCAGTGGCAGCAGCAGGAGCTCACCAAGACCCACAGCAGGACATTCAGA	Db 538 GCGAGCAC
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RESULT 5
US-10-660-763-3
; Sequence 3, Application US/10660763
; Publication No. US20040063130A1
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TYPE: DNA
CORGANISM: Homo sapiens
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APPLICANT: GAN, WEINIU et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1183DIV
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity
Matches 363; Conserv
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Pred. No. 1.2e-46;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1503
LENGTH: 449
TYPB: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                            US-09-918-995-1503
Sequence 1503, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Sim Matches 363;
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TITLE OF INVENTION: ISCLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TILE REFERENCE: CL001183DIVII
CURRENT APPLICATION NUMBER: US/10/660,763
CURRENT FILING DATE: 2003-09-12
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TYPE: DNA
ORGANISM: Homo sapiens
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Similarity 99.7%;
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Pred. No. 1.2e-46;
0; Mismatches 1
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(449)
OTHER INFORMATION: n = A,T,C
-09-918-995-1503

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Sequence 5, Application US/09948802

Publication No. US20020172981A1

GENERAL INFORMATION:

APPLICANT: ROBISON, KEITH E.

ITITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR FILE REFERENCE: MNI-090

CURRENT APPLICATION NUMBER: US/09/948,802

CURRENT PILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: 09/387,212

PRIOR APPLICATION NUMBER: 09/387,212

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 18

SOPTMARE: PALENTIN Ver. 2.0

SEQ ID NO 5

LENGTH: 361
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US-09-948-802-5
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: All occurences of n indicate any nucleotide
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ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1981
                                                          CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA 1923
                                                                                                                                             TCCGCACGGAGGGGCCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAG 1863
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                                  CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA 259
                                                                                                            TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG
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Pred. No. 2.2e-41;
0; Mismatches 2; Indels 0;
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Sequence 5, Application US/10121925

Publication No. US20030104505A1

GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH E.

ITILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR FILLE REFERENCE: MAI-090

CURRENT APPLICATION NUMBER: US/10/121,925

CURRENT FILING DATE: 2002-04-12

PRIOR APPLICATION NUMBER: US/09/948,802

PRIOR APPLICATION NUMBER: US/09/948,802

PRIOR FILING DATE: 2001-09-07

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0
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US-10-121-925-5
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LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: All occurences of n indicate any nucleotide
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Best Local Similarity
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Pred. No. 1.1e-36;
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US-10-280-576-19
; Sequence 19, Application US/10280576
; Publication No. US2004004405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COFFILE REFERENCE: 09820.189
; CURRENT FILING DATE: 2002-10-22
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732

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; PRIOR FILING DATE: 2001-10-25; NUMBER OF SEQ ID NOS: 25; SOFTWARE: PatentIn version 3.1; SEQ ID NO 19; LENGTH: 1779; TYPE: DNA; ORGANISM: Drosophila melanogaster US-10-280-576-19
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Best Local Similarity
Matches 518; Conserv
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                              ATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAG
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Pred. No. 8.5e-33;
0; Mismatches 384
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; ORGANISM: Homo sapiens
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SEQ ID NO 525
LENGTH: 3875
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Best Local Similarity 54.9%;
Matches 423; Conservative
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APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CCURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
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Pred. No. 6.6e-22;
0; Mismatches 338;
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PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: DE 10155280.7
PRIOR FILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 173
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Best Local Similarity 54.7%;
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SEQ ID NO 1
LENGTH: 2955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
TITLE: Eph Al
PATENT DOCUMENT NUMBER: NM00532
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 20200/2002
CURRENT APPLICATION NUMBER: US/10/384,339C
CURRENT FILING DATE: 2003-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/EP02/00152
PRIOR FILING DATE: 2002-01-09
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                                                                                                                                                                                CGATCATGATCACAGAATTTATGGAGAATGCAGCCCTGGATGCCTTCCTGAGGGAGC 2173
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                   TGAACTACCTCAGTAATCACAATTATGTCCACCGGGACCTGGCTGCCAGAAACATCTTGG
                                                         TGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGCCTGG 1932
                                                                                                   GGGAGGACCAGCTGGTCCCTGGGCAGCTAGTGGCCATGCTGCAGGGCATAGCATCTGGCA
                                                                                                                               AGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCTGGCA 1872
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Pred. No. 2e-21;
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; ORGANISM: Homo sapiens
US-09-967-768A-144
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APPLICANT: AUGUSTUS, Meena
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-72
CURRENT APPLICATION UNMERR: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0
SEQ ID NO 144
LENGTH: 3370
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Best Local Similarity 54.7%;
Matches 421; Conservative
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PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
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                                    CCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGGGGCGACTTCCTGACCTTCCTCCGCACGG 1812
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CGATCATGATCACAGAATTTATGGAGAATGCAGCCCTGGATGCCTTCCTGAGGGAGC
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AGCTCATGAAGAACTGCTGGGCATATGACCGTGCCCGCCGGCCACACTTC
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Therapeutic Screening Using Signatur

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FILE REFERENCE: MPIO2-020PIRNOWNIM
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR PILLING DATE: 2002-01-31
PRIOR PILLING DATE: 2002-01-31
PRIOR PILLING DATE: 2002-03-15
PRIOR PILLING DATE: 2002-04-09
PRIOR PILLING DATE: 2002-04-09
PRIOR PILLING DATE: 2002-04-10
PRIOR PILLING DATE: 2002-04-10
PRIOR PILLING DATE: 2002-04-16
PRIOR PILLING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR PILLING DATE: 2002-04-16
PRIOR PILLING DATE: 2002-04-16
PRIOR PILLING DATE: 2002-04-16
PRIOR PILLING DATE: 2002-04-19
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US-10-354-358-101
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APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Hunter, John Joseph
APPLICANT: MacBeth, Kyle J.
APPLICANT: Teai, Fong-Ying
APPLICANT: Lesoon, Andrea
APPLICANT: Lightcap, Eric S.
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Williamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 885269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33220, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
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PRIOR FILING DATE: 2002-06-14
PRIOR PPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
Remaining Prior Application data removed - Se.
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 82
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Publication No. US20040132086A1
GENERAL INFORMATION:
APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relate
TITLE OF INVENTION: Thereto
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Best Local Similarity
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CURRENT FILING DATE: 2004-02-10
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ORGANISM: Homo sapiens
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                                      GGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGG 2052
                                                                                                            TGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTTGGGATGTCCCGAGAGGGAAGCCGATG
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Search completed: March 19, 2005, 19:55:48 Job time : 1398.78 весв	2233 GGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTC 2282	2173 AGTTTGTGGAGAAGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCA 2232	2113 GGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGG 2172	2053 CCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCT 2112

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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B1 TCAGCACCATCTACCAGAGCTGCAGAGCATCCGAAAGCGGCATCGGTGAGGCTGGGAGCCTGGAGCATCCGATAGGCTGGAGGCTGGGAGCCTGGAGGCTGGGAGCATCCGAAAGCGGCATCGGTGAGGCTGAGGCTGGGACGCTGAGGCTGGGACCATCGGAAGCGGCATCGGTTGAGGCTGGGACGCTGGGACCATCGGAAGCGGCATCGGTTGAGGCTGGGACCATCGGAGCTTGAGGCTGGGACCATCGGAAGCGGCATCGGTTGAGGCTGGGACCATCGGACGCTGAGAGCATCGGAAGCGGAAAGCGGCATCGGATCAGAGCTGAGAGCATCGAAAGCGGCATCGGATCAGAGCATCAGAGAGCATCAGAGCTGAAGAGCAACAAGAGCAATCAGAAGCGGAATCAGAAGCGAATCAGAAGCGAATCAGAAGCGGAATCAGAAGCGAATCAGAAGCGAATCAGAAGCGAATCAGAAGCGAATCAGAAGCGAATCAGAAGCAATCAGAAGCGAATCAGAAGCGAATCAGAAGCGAATCAGAAGCGAATCAGAAGCGAATCAGAAGCAATCAGAAGCAATCAGAAGCAATCAGAAAGCGAATCAGAAGCAATCAGAAGCAATCAGAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAGCAATCAGAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAAGCAATCAGAAAGCAATCAGAAAGCAATCAGAAAAGCAATCAGAAAGCAATCAGAAAAGCAATCAGAAAAGCAATCAGAAAAGCAATCAGAAAAGCAATCAGAAAAGCAATCAGAAAAGCAATCAGAAAAGCAATCAGAAAAAAAA	рь	1201 TGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCC 1260	유 왕
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Sequence 1, Application US/10003295
; Sequence 1, Application US/10003295
; Retent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: 1601ATED HUMAN KINASE PROTEINS, NUC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINA
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; ENOTH: 2674
; TYPE: DNA
; ORGANISM: Homo Sapiens
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RESULT 3
US-09-817-180-3
; Sequence 3, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:

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Sequence 3. Application US/10003295

Sequence 3. Application US/10003295

Patent No. 6686187

Patent No. 6686187

PAPLICANT: GAN, Weiniu et al.

APPLICANT: GAN, Weiniu et al.

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001183DIV

CURRENT APPLICATION NUMBER: US/10/003,295

CURRENT FILING DATE: 2001-12-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 15297

TYPE: DNA

ORGANISM: Homo sapiens

US-10-003-295-3
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US-10-003-295-3
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THERBOF
FILE REFERENCE: CLOO1183
CURRENT APPLICATION NUMBER: US/09/817,180
CURRENT FILLNG DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15297
TYPE: NUMBER: 15297
                                 Query Match
Best Local Similarity
Matches 363; Conserv
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Best Local Similarity 99.7
Matches 363; Conservative
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TYPE: DNA
ORGANISM: Human
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99.7%;
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Pred. No. 5.1e-55;
0; Mismatches 1;
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                                  Score 362.4; DB 4; pred. No. 5.1e-55; 0; Mismatches 1;
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RESULT 5
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US-09-387-212-5
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GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH E.
TITLE OF INVENTION: NUCLEIC ACID M
TITLE OF INVENTION: PHOSPHATASE HO
                                                                                                                                                                                                                                                                                                                                             Query Match 11.1%;
Best Local Similarity 97.4%;
Matches 333; Conservative
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SEQ ID NO 5
LENGTH: 361
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CURRENT APPLICATION NUMBER: US/09/387,212A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
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                   ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1981
                                                                                        CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA
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VENTION: NUCLEIC ACID MOLECULES

VENTION: PHOSPHATASE HOMOLOGUES
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Pred. No. 1.1e-43;
0; Mismatches 4
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US-09-948-802-5
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Best Local Simil
Matches 333; (
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CURRENT APPLICATION NUMBER: US/09/948,802
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5.
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Patent No. 6465232
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROBISON, KEITH E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE
TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                 1982
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 GGAAGCCCGATTGGGGGTCTATGCAGCCTCAGGGGGCCTCAG
                                                                   ACTGCCTGGTGACAGAAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA
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Pred. No. 1.1e-43;
0; Mismatches 4;
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RESULT 7

US-09-949-016-12110
US-09-949-016-12110
Sequence 12110, Application US/09949016
Sequence 12110, Application US/09949016
Sequence 12110, Application US/09949016
Settle No. 6812339
GENERAL INFORMATION:
APPLICATI: VENTER, J. Craig et al.
APPLICATI: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,498

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; SEQ ID NO 15795
; LENGTH: 19153
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15795
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAKISEQ for Windows
SEQ ID NO 12110
LENGTH: 19152
TYPE: DNA
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Best Local Similarity
Matches 224; Conserva
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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CGGGTCAAĜAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGT
                                                                                                        CAGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGCCATGAGAAAGTGGATGGCCCAG
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                                              CGGGTCAAGAGTGACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGT
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ilarity 99.6%;
Conservative
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Pred. No. 2.4e-30;
0; Mismatches 1;
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Pred. No. 2.4e-30;
0; Mismatches 1
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APPLICANT: Horwitz, Kathryn
APPLICANT: Horwitz, Jennifer
TITLE OF INVENTION: Thereto
FILE OF INVENTION: Thereto
FILE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SQFTWARE: Patentin version 3.1
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US-09-814-915A-82
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GENERAL INFORMATION:
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Best Local Similarity 54.7%;
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GGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGG
                                                                                                        CCCTTAACTACGGCCGCTACTCCGAAAGCGAACGTGTGGAGCTTTGGCATCTTGCTCT
                                                                                                                                                                            TTGATGGCACATACGAAACCCAGGGAGGAAAGATCCCTATCCGTTGGACAGCCCCTGAAG
                                                                                                                                                                                                                                   GGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGG
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Pred. No. 5e-26;
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APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-09-08
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US-09-949-016-628
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Best Local Similarity 55.1%;
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APPLICANT: VENTER, J.
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                                                                                                                                                                                AAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCCGAAAGCGACGTGTGG
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                                                                                                                                  CGCTGGACCGCCCCGGAGGCCATTTCCTACCGGAAGTTCACCTCTGCCAGCGACGTGTGG
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2120
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US-09-949-016-2120
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Best Local S
Matches 385
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Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2120
LENGTH: 3921
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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AAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGG
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                                                                                                           CGAGAGGAAGCCGATGGGGTCTATGCAGCCT---CAGGGGGCCTCAGACAAGTCCCCGTG 2033
                                                                                                                                                       GCCCGCAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCTGACTTTGGCCTGTCC
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ilarity 55.1%;
Conservative
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RESULT 12
US-09-949-016-5662
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SEQ ID NO 5662
ELENGTH: 3386
TYPE: DNA
ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Best Local
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                     1809 ACGGAGGGGCCCCCCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCT 1868
                                                                                                                                                                                                                                                                                                      1506 ATCATGAAGAACCTCGACCACCCGCACATCGTGAAGCTGATCGGCAT----CATTGAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392;
                                                                                                 GGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGC 1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGAGGTCTATGAAGGTGTCTACACAAATCACAAAGGGGAAAAATCAATGTAGCTGTC 1445
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CTGGTGACAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCC 1988
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                                                  GCCATGGCCTACCTGGAGAGCATCAACTGCGTGCACAGGGACATTGCTGTCCGGAACATC
                                                                                                                                                      CGGAACAAGAACTCCCTGAAGGTGCTCACCCTCGTGCTGTACTCACTGCAGATATGCAAA 1682
                                                                                                                                                                                                                                                       GAGCCCACCTGGATCATGGAATTGTATCCCTATGGGGAGCTGGGCCACTACCTGGAG 1622
                                                                                                                                                                                                                                                                                                                                                                                                        ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCCCCTCCGCCATCTACCAGCTCATGATGCAGTGCTGGCAGCAGGAGCGTGCCCGCCGC 2696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGG
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Mismatches
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RESULT 13
US-08-357-642A-2
US-08-357-642A-2
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APPLICANT: Sima Lev

APPLICANT: Joseph Schlessinger

TITLE OF INVENTION: PYK2 RELATED

TITLE OF INVENTION: AND METHODS

TITLE OF SECUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08357642A Patent No. 5837524
                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US
FILING DATE: December
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                     STRANDEDNESS:
TOPOLOGY: 1i1
MOLECULE TYPE:
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPUTER: IBM P.C.
OPERATING SYSTEM: IBM P.C.
CORTWARE: Word Perfect 5.1
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STREET: 633 West Fifth
STREET: Suite 4700
                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                               ENGTH:
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GENERAL INFORMATION:

APPLICANT: SIMA LEV

APPLICANT: JOSEPH SCHLESSINGER

APPLICANT: JOSEPH SCHLESSINGER

TITLE OF INVENTION: PYK-2 RELATED PR

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

ADDRESSEE: Lyon & Lyon
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US-08-460-626-2
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COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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0; Mismatches 319;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416
Type
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Best Local Similarity 54.7%;
Matches 392; Conservative
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FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/357,642
FILING DATE: December 15, 1994
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600 TELEFAX: (213) 955-0440
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OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
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STRANDEDNESS: single
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      ATCGGGGTGCTGGAGAAAGGAGACCGGCTGCCCAAGCCTGATCTCTGTCCACCGGTCCTT
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                                               CTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACA 2168
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US-09-016-434-1483
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REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1483:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
PILING DATE: HEREWITH
CLACOTTOM
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Best Local Similarity 54.7%;
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 94304
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                                                                                                                                                                    1629 AAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGG
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ATCATGAAGAACCTCGACCACCCGCACATCGTGAAGCTGATCGGCAT----CATTGAAGAG
                                                                            ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTTCTGCACCCAGAAG
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                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                           Score 174.6; DB 4; Length Pred. No. 7.1e-22; O; Mismatches 319; Indels
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                   41 CCAGGAGCAGCTGCCCGTGCGGAACAGCACTATGGGCTTCTCTTCTGAGCTGTGCAGCCC
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invityogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 2461)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2461 bp mRNA linear full-length cDNA clone CSODIO69YK21 of Placenta Cot of Homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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HTC; CNSLT_CDNA.
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QY 1947 GTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGGAAGCCGATGGGGTCTATGCAGCC 2006	Qy 1887 AGCAAGTGCTGCATCCACCGGGACCTGGCTGGCTGGCTGG	Qy 1827 CGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAG 1886	Qy 1767 ATGGAGCTTGTGCAGGGGGGGGGGGCTACCTTCCTTCCTCCGCACGGAGGGGGCCCGCCTG 1826	OY 1707 CACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTC 1765	QY 1647 CTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGC 1706			1467 CCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCCCAAGGACAAGTGGGTGTGCTGTGCCTGTGCCCAAGGACAAGTGGGTGTGTGCTGTGCTGTGCTGTGCTGTGCTG	1407 GANGGGINTCCTRGCATTCCTTTGCTCATCGACCACCTACTGGACCACCCAGCAG	1591 1561 CCCCTCAGAATGGAGGCTGCCTGACCCCGGGTCCCCTGCCCTGCAGAACCTGTACCGACTG	1501 GTACGTGCTGTCGGTGCTGTGGGATGGTCTGCCCCGGCACTTCATCATCCAGGCTCACGC	Db 1441 GGCTGAGCTGCTGGTGCACTCTGGGGACTTCCTGGTGCGGGAGAGCCAGGGCAAGCAGGA 1500 Qy 1391 1390	Db 1381 GGTGCAGAAGCCCCTGCATGAGCAGCTGTGGTACCACGGGGCCATCCCGAGGGCAGAGGT 1440 Oy 1391 1390	Qy 1391 1390	QY 1361 CATCTCAGGAATCTTCCGCCCCAAGTTCTC	QY 1301 GTCCTCGGAGCAGGAGCGAGAGGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCA 1360		

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Query Match 44.5%; Score 1189; DB 3; Length 1189; Best Local Similarity 100.0%; Pred. No. 2.1e-201; Matches 1189; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1326 GGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAG 1385		- FRANCE (E-mail: segref@genoscope.cns.fr 18.fr) 18	Unpublished Contact: Feng Liang Email: fliang@lifetec http://fulllength.invitrogen.com/ InVitroGe Faraday Avenue 2 (bases 1 to 1189) Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre		CR533571 GI:50474764 CR533571 GI:50474764 HTC; CNSLT_CDNA. Homo sapiens (human)	CR593957 1189 bp mRNA linear HTC 21-JUL-2004 ON full-length cDNA clone CSODI008YG07 of Placenta Cot 25-normalized of Homo sapiens (human).	2367 GGCC 2370 2458 GGCC 2461	2307 AGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA 2366	2247 TGCTGGGCCTATGAGCCTGGGCACGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG 2306	2187 GGGGGCCGTCTGCCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG 2246	2127 CTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAG 2186 2278	2067 CGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGC 2126 2278 2277	
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2346 CTCAAGCTGGTGGCCTCTGCAGGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCATATGC 2405	2226 GTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGC 2285	2106 TICCTCTGGGAGACCTTCAGCCTGGGGGGCTCCCCCTATCCCAACCTAACAATCAGCAG 2165 2107	1946 GCUARIGGGTCIAIGCAGCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTCGAACTCA 2043 [TGCCTGGTGACAGAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAA	481 CGCACGGAGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCT 540 1866 GCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAAC 1925	AAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGG	1686 AGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAG 1745	1626 GTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCG 1685 	1566 CGGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCCTGGTGGCG 1625	1506 GTGCCCAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGA 1565	1446 CACCTACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCT 1505	1386 TICTOGAACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCATTCCTTTGCTCATCGAC 1445	

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On May 5, 2003 this sequence version replaced gi:30372027.
Contact: Genoscope
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BX356089 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI008YG07 5-PRIME, mRNA sequence.
BX356089
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1 (bases 1 to 936)
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                                                                                                                                                                                                                                                                                                                                                                                             GGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAG
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                              CGGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACACCCTGGTGGCG 1625
                                                                                            GTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTGGGTGAGCAGATTGGA 240
                                                                                                                                                GTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGA 1565
CGGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCCTGGTGGCG
                                                                                                                                                                                                 CACCTACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCT
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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RESULT 4 BX356089/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	D 09 5	ο _γ 2	Qy 2	рь Qy 2	Qy 1	Qy 1	Qy 1	Qу 1 Db	Оу ръ	Qу 1 Db	Qy
BX356088 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO08YG07 3-PRIME, mRNA sequence. BX356088 EX356088 2 GI:46288403 EST. Homo sapiens (human) Homo sapiens (human) Homo sapiens (constant) Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 980) Li,W.B., Gruber, C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization Unpublished (2001) On May 5, 2003 this sequence version replaced gi:30369992. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: sequence cons.fr. Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster	225 CGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGA 2260	2165 GACACGGGAGITTTGTGGAGAAAGGGGGGCCGTCTGCCCCTGCCCAGAGCTGTGTCCTGATGC 2224	1106 TIGCTCIGGGAGACCTTCAGCCT-GGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCA 2164	2046 CCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATC 2105	1986 GCCGATGGGGTCTATGCAGCCTCAGGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCA 2045	926 TGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAA 1985 	866 GCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGG	1806 CGCACGGAGGGGCCCCCCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCT	1746 AAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGACTTCCTGACCTTCCTC 1805	1616 AGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAG 1745	در در

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                             GGCCTATGAGCCTGGGCAGCGGSCCAGCTTCAGCACCATNTAMCAGGAGCTGCAGAGCAT
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-cligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
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                                                                           Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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3373 bp mRNA linear HTC 03-API Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200003015 product:similar to PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) [Mus
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Pukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiranoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, I
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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[AL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.jp/) for further details.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
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Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30548660.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the Not I and EcoRV sites of the pcWVSpORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 7663.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE013DH01QP1&c=7663.f.
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5-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 936)
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                                                           ACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGTGACAGGGAGTATGCAGG
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/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/clone Tib="Homo sapiens PLACENTA"
/clone_Tib="CDNA was primed
with a NotI-oligo(dT) prImer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and Ecory sites of the pCMVSPORT 6 vector.
Library was not normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                               Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.go
Tissue Procurement: ATCC
                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AGENCOURT 6403957 NIH MGC 92
5', mRNA sequence.
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cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.E. Consc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCCAGCG
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                                       GAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCA
                                                                                                                                                                                                    GCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGCTACCA
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CCAGCACCACCAGCTCCTGCTGCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGA
                                                               GAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCA
                                                                                                          GGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTG
                                                                                                                                 GGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCCAAGGACAAGTATGTGCGCAGCCTGTG
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Location/Qualifiers
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/db xref="taxon:9606"

/clone="IMAGE:5583652"

/tissue_type="embryonal carcinoma, cell line"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_92"

/clone_tib="NIH_MGC_92"

/clone_Torgan: testis; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: Sall; Cloned unidirectionally; oligo-dT_primed.

Average insert size 2.5 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."
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|mol_type="mRNA"
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Pred. No. 1.2e-145;
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CCAGCACCACCACCAGCTCCTGCTGCCCGGNCTGCTGCGGTCACTGCAGGACCTGCACGA

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                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                    division of Invitrogen
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 863)
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Homo sapiens (human)
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                  CGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCT
                                                                                    AAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTC
                                                                                                                                                         AGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAG
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 CGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCT
                                                                 AGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAG
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                                                                                                                                                                                                32.3%; Score 863; DB 3; Le larity 100.0%; Pred. No. 2.3e-143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
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/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
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Homo sapiens (human)

[SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 989)

El (bases 1 to 989)

El (w.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

NLU (npublished (2001)

On May 5, 2003 this sequence version replaced gi:30376296.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CF 5706 - 91057 ERRY cedex - FRANCE

Email: sequefegenoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
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BX359009
BX359009.2 GI:46305682
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                                                        ACACGGGAGTTTGTGGAGAAGGGGGGCCGTCTGCCCCTGCCCAGAGCTGTGTCCTGATGCC
                                        ACACGGGAGTTTGTGGAGAAGGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCC
                                                                                                 TTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAG
                                                                                                                           TTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAG 2165
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO51BH10NP1&c=7663.f.
                                                                                                                            GCCGATGGGGTCTATGCAGCCTCAGGGGGGCCTCAGACAAGTCCCCCGTGAAGTGGACCGCA
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Best Local Similarity
Matches 858; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 7663.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE004CG05QPl&c=7663.f.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001) on Peb 15, 2001 this sequence version replaced Contact: Genoscope
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AL540776
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 861)
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                                                                                                  Conservative
                                                                                                                                                                                 /tissue_type="PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector: pcfW/SpOrT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                        clone="CSODE004YN09"
                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                     xref="taxon:9606"
                                                                                                                  31.3%;
99.4%;
                                                                                                 Score 836.6; DB 1;
Pred. No. 1.1e-138;
2; Mismatches 1;
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Bukaryota, Metazoa; Chordata; Craniata; Verteb Mammalia; Butheria; Primates; Catarrhini; Homi 1 (bases 1 to 968)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length CDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                  BX359010 968 bp mRNA linear ES BX359010 Homo sapiens PLACENTA COT 25-NORWALIZED Homo clone CS0DI051Y020 5-PRIME, mRNA sequence.
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO51BH10QP1&c=7663.f. Location/Qualifiers
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                                                                                                CCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATGTGC
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                                                                    CCAAGGACAAGTATGTKCGCA-CCTGTNGAAGCTCTTTGCTCACCACAACCGCTATGTGC
                                                                                                                                                                     ACAGTGCCCAAGCCAAGCTTCCAGGAGGCCAGCAAAGACAAGGACCGTGACAAGG
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
/clone="CSODI051YO20"
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Pred. No. 5.4e-136;
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AGGATCCTGAAGCAGAACAGCCACCCCAACTTCGTGCGTCTCATTGGTTTCTGCACCCAR

789

Local Similarity

Conservative

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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime
1st strand cDNA was digested with Not I and cloned
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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1 (bases 1 to 848)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:30544304.
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AL540775 AL540775
AL540775 AL540775
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                                                                                                         /tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned ithe Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                        clone="CS0DE004YN09"
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                       30.1%;
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Pred. No. 4.8e-133;
1; Mismatches 15;
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1 (bases 1 to 939)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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division of Invitrogen. This sequence belongs to sequence cluster
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On May 8, 2003 this sequence version replaced
Contact: Genoscope
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       GCGGGCTGCGCAGCTACACCACCAGCACCAC - CACCAGCTCCTGCTGCCCGGCCTGCTGC
                                                                    CAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGT
                                                                                                                                                                                                          CCACAGCCCAGGACATTGAGAAGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGC
                                                                                                                                                                                                                                                                            GCAGCTTCGCAAGACCTACAGCGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAGAC
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                                          CAAGTATGTGCGCA-CCTGTGGAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGT
                                                                                                                 CCAAGCCAAGCGCAAGTACCAGGAGGCCAAGCAAAGACCAAGGACCGTGACAAGGCTAAGGA
                                                                                                                                                CCAAGCCAAGCGCAAGTACCAGGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCCAAGGA
                                                                                                                                                                                     CCACAGCCAGGACATTGAGAAGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGC
                                                                                                                                                                                                                                                            GCAGCTTCGCAAGACCTACAGCGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAGAC
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
/clone="CSODI069YK21"
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; Pred. No. 6.3e-133;
13; Mismatches 4;
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Best Local Similarity
Matches 850; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope - Centre National de Sequencage
2 rue Gaston Cremteux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 913)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:30606435.

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL569718 Homo sapiens PLACENTA Homo 3-PRIME, mRNA sequence.
AL569718 AL569718 AL569718 GI:46235981
                                                                                                                                                                                                                                                                                                                                                                                                                   For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE013DH01NP1&c=7663.f. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence belongs to sequence cluster 7663.f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
       ACCTGACCTCAAGGCCAAGTTT-CTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACC
                                                                 GGACGCCTGCGAGCCGACAACACCCCTGGTGGAGGTGAAGTC-TTGTCGAGAGACGCCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGCACCTGACGTCCCACCCTGTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCTGCTGCCCGCATCCAGCCTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGT
                                          GGACGCCTGCGAGCCRACACACCCTGGTGGCGATGAAGTCTTTGTCGAGAGACGCTCCC 854
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                                                                                                                 Conservative
                                                                                                                                                                                                   /tissue_type="PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Woctor: pcfW/SpORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE013YP02"
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                                                                                                                                29.6%;
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                                                                                                             Score 791.6; DB 1;
Pred. No. 1.2e-130;
7; Mismatches 27;
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sapiens cDNA clone CS0DE013YP02
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                                                                                                                                                                 5', mRNA sequence.
BQ708270
BQ708270.1 GI:2184
EST.
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Homo sapiens (human)
Homo sapiens
Edwaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
1 (bases 1 to 948)
11 (bases 1 to 948)
11 (MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                    948 bp
AGENCOURT_8484911 NIH_MGC_113 Homo
                                                                                                                                                                                                                                                                                                                                                                 TCCTGCCACCAGCATCCACACTGCCGGCAGGATGCAGCGCCGTGTCCTCTCTGTGTCCC
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                                                                                                                                                                                      GI:21847169
                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                           mRNA
                                            Gene Collection (MGC)
                                                                                                                                                                                                                                        linear EST 16-JUL-2002 CDNA clone IMAGE:6301278
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FEATURES
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Best Local Similarity >...
818; Conservative
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Tissue Procurement: Dr. Mark Matson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2516 row: o column: 07
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Location/Qualifiers
  ATCCAGCCTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTC
                                                                                                                                                                                                                                                                     CTACACCACCAGCACCACCAGCTGCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGAC
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                                                                              AGCCTGGTGCAGGATGAGGTGGTGGCCGTCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGC
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                                                AGCCTGGTGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MCC_111"
/clone_lib="NIH_MCC_111"
/clone_"organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAe(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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95.3%;
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Pred. No. 4.3e-127;
0; Mismatches 34;
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841	1128	781	1072	721	1014	661	954	601
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Search completed: March Job time: 7733.14 secs 19,

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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     1553
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Match
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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ADQ54298
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Aba94500 Human pro
Abv75413 Human kin
Adm28580 Human pro
Adk71888 Human kin
Aas95001 Human DNA
Adr39816 Human kin
Ada43980 CRAM prot
Aan70060 fes/fps p
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Adq54298 Novel can
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Ad171054 Human pro
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Ad61604 Human pro
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Abx14976 Human pro
Abx14976 Human pro
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Human proto-oncogene tyrosine kinase encoding cDNA

09-APR-2002 (first entry)

ABA94500;

ABA94500 standard; cDNA; 2674 BP.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
185.4	185.4	185.4	185.4	185.4	185.4	185.4	185.4	185.4	198	198	198	198	198	198	198	198	198	198	199.2	199.6	201.2		271.6	271.6
6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.5	7.5	7.5	10.2	10.2
3921	3921	3921	3919	3346	3042	3042	3042	3042	3370	3370	3370	3370	3370	3370	2955	2955	2955	2955	2778	5616	3875	3286	3369	3198
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ADB37439	ABZ34865	ABV94231	ACN37278	ACN42099	ABL91659	ABX09937	ABZ35694	ABV78118	ADQ80244	ADJ75094	ADE38440	ADD18447	ABZ34861	ABL67952	ABL91658	ABX09936	ABZ35693	ABV78117	ADP28218	ADE08824	ABZ35414	ADK71885	ABL14457	ABL18403
Adb37439 Human can	Abz34865 Coding se	Abv94231 Breast ca	Acn37278 Tumour-as	Acn42099 Human dia	Abl91659 Human pol	Abx09937 Human eph	Abz35694 Human eph	Abv78118 Human eph		Adj75094 Marker ge	Ade38440 Human pro	Add18447 Human pro	Abz34861 Coding se	Abl67952 Ovary can	Abl91658 Human pol	Abx09936 Human eph	Abz35693 Human eph	Abv78117 Human eph	Adp28218 Human sec	Ade08824 Novel DNA	Abz35414 Human gen	Adk71885 Human kin	Abl14457 Drosophil	Abl18403 Drosophil

ALIGNMENTS

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RESULT 1
ABA940
ABA940
XX ABA9
XX ABA9
XX Prot
XX Prot
XX Prot
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XX Prot
XX Prot
XX ABA9
XX Prot
XX Prot
XX ABA9
XX Prot
XX Prot
XX CDS
FT CDS
FT S'UT
FT 3'UT
FT 3'UT
FT 27-M
XX CDS
FT CDS
FT GGan
XX WPI;
DR WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proto-oncogene tyrosine kinase; poTK; tumour; cytostatic; anti-leukemic; gene therapy; protein therapy; vaccine; enzymatic-inhibition; human; anti-kinase; ss.
              Nucleic acids encoding a proto-oncogene tyrosine kinase, useful for the prevention, diagnosis and treatment of e.g. leukemia and lung tumors.
                                                           WPI; 2002-138497/18.
P-PSDB; ABB07354.
                                                                                                        Gan W,
                                                                                                                                                                                                                                                                                                            3'UTR
                                                                                                                                                                                                                                                                                                                                                                                      5'UTR
                                                                                                                                                                    27-MAR-2001; 2001US-00817180
                                                                                                                                                                                                 27-MAR-2001; 2001US-00817180.
                                                                                                                                                                                                                                 22-JAN-2002.
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                                                                                                                                       (PEKE ) PE CORP NY.
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72. .2330
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/*tag= b
/2331. .2674
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                                                                                                        Beasley EM;
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Query Match
Best Local Similarity
Matches 2674; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2674 BP;
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                                                                                                                                 Matches 2674;
                                                                                                                                                   Query Match
Best Local Similarity
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5'UTR
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06-DEC-2001;
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The invention relates to a new isolated human proto-oncogene tyrosine kinase peptide or its allelic variant, orthologue or fragment. The peptide is useful for preparing a composition for treating a disease or condition mediated by a human kinase protein e.g. cancer. The present
                                                       Claim 4; SEQ ID NO 1; 53pp;
                                                                               New human kinase peptides, useful for preparing a treating a disease or condition mediated by human
                                                                                                                  WPI; 2004-282461/26.
P-PSDB; ADM28581.
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                                       GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCC
                                                                     CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCT
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ADK71888 standard; CDNA; 2599 ВÞ

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20-MAY-2004 (first entry)

Human kinase and phosphatase KPP-6 cDNA

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XX Anti:
XX An dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antipheumatic; antiparkinsonian; nootropic; antiparkin; hepatotropic; antipheumatic; antibacterial; virucide; protozoacide; fungicide; antibacterial; virucide; protozoacide; fungicide; cardiovascular disease; immune system; neurological; growth; development; cell proliferation; viral; bacterial; fungal; parastic; protozoan; helminthic infection; transgenic; gene therapy; ss; gene; single nucleotide polymorphism; SNP. human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV; antiallergic; antiasthmatic; immunosuppressive; antithyroid;

Homo sapiens

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Key variation Location/Qualifiers
replace(109,T)
/*tag= a
/label= Single nucleo a Single nucleotide polymorphism

(SNP)

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The invention relates to a novel isolated polypeptide which is a human CC kinase and phosphatase (KPP). The polypeptide of the invention CC demonstrates cardiovascular, antiarteriosclerotic, hypotensive, CC vasotropic, antiinflammatory, antianginal, anti-HTV antiallergic, CC antiasthmatic, immunosuppressive, antithyroid, dermatological, neuroprotective, antiasthmatic, antiprotropic, antigout, gastrointestinal, neuroprotective, CC antidabetic, nephrotropic, antigout, gastrointestinal, neuroprotective, antiparatic, ophthalmological, antipsoriatic, controparatic, ophthalmological, antipsoriatic, antipsoriatic, antiparasitic, antipsoriatic, antiparasitic, antipsoriatic, cc antibacterial, virucide, protrozoacide and fungicide activities. The CC kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and cardiovascular diseases, immune system disorders, disorders affecting growth and development, cell protozoan or helminthic infections. Furthermore, the molecules of the CC invention may be useful for creating transgenic animals to model human CC disease and during gene therapy. The current sequence is that of a human cxx
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 2537; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT; Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ; Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA; Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Murage J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
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25-SEP-2002; 2002US-0411910P.
27-SEP-2002; 2002US-0414296P.
11-OCT-2002; 2002US-0417821P.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Matches 2558
                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. ANS94746-ANS9521 represent the human polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
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1771 AGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGGCCCGCCTGCGGG	01 GTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCC 9	용 ઇ
1711 CCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCGACTACATCGTCATGGT 	QY 841 CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCT 900	B &
1651. CACCTGACCTCAAGGCCAAGTTTCTACAGGAGGAGTCCTGAAGCAGTACAGCCACC	81 TGCAGGATGAGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCGCATCCAGC 840	B 8
	721 AGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGG 780	8 8
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	541 AGGAGGCCAGCAAAGACCAAGGACCAAGGACAAGGACAAGGACAAGGACCAGCCTGT 600	<u> </u>
	481 AGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGTACC 540	문 원
1618 CTGGGGACTTCCTGGTGCGGGAGAGCCAGGGCAAGCAGGAGTACGTGCTGTCCAGTGCTGT	421 GCGAGCAGTGGCAGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGA 480	B 8
1558 AGCAGCTGTGGTACCACGGGGCCATCCCGAGGGCAGAGGTGGCTGAGCTGCTGGTGCACT	361 GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACA 420 Db	
	302 CAGCCAAACTGA-GGGCCTGAGCCGCTTGCTGCGGCAGCACCACAGAGGATCTGAACTCAG 360 Do	<u> </u>
1321 AGGGGGAAACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCGGCC 1438 AGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCC 1438 AGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCCAGGAATCTTCCGCC	242 GGGCCAGAGCCGGGCCCATCAGCCCCTGACAGCCCCATCAGTCAG	용왕
	182 GGTCAAGAGTGACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGG 241	<u> </u>
1318 TGCCTCTCTCTCTCTCCAGGATTGCTCCAGCCTCCTCTTCTTCTAGGAGCAGGAGCAGGATTGCTAGGATTGCTAGGATTGCTAGGATTGCTGCAGGATTGCTTCTTCTAGGATTGCTAGGATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAGATGA	122 GCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCG 181	8 8

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19-MAR-2003;
28-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; gene therapy; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; developmental disorder; Hypothyroidism; Cushing's syndrome; infection; KPP-43; single nucleotide polymorphism; SNP; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR39816 standard;
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2003US-0456932P
2003US-0458844P
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replace(109,C)
/*tag= b
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CC invention have cytostatic, antiarteriosclerotic, anti-HTV, antiallargic, concerns, neuroprotective, cerebroprotective, anti-HTV, antiallargic, concerns, and thyromimetic activities, and can be used in gene therapy. The human KPP proteins and polymucleotides can be used in the decreased human kPP proteins and polymucleotides can be used in concerns, atherosclerosis, neurological (e.g. atherosclerosis), neurological (e.g. AIDS, allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome) confections. They can also be used in ascessing the effects of exogenous compounds on the expression of nucleic acid and amino acid compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                            New human kinases and phosphatases (KPP) for diagnosing, treating and preventing diseases or conditions associated with aberrant KPP expresses; cancer, acquired immunodeficiency syndrome, epilepsy, or infecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ramkumar J, Marquis JP, Swarnakar A, Chawl
Becha SD, Lee SY, Hafalia AJA, Richardson
Jackson AA, Yang J, Gorvad AE;
Sequence 2623 BP;
                                                                                                                                                                                                                                                                                                                                                                                           Claim 5;
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17-APR-2003; 2003US-0463937P.
                                                                                                                                                                                                                                                                                                                                  present sequence encodes the human kinase and P), designated KPP-43. The human KPP sequences
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 89;
541 A; 786 C; 840 G; 456 T; 0 U; 0 Other;
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Query Match 73.0%; Score 1953; DB 13; Length 2623; Best Local Similarity 85.8%; Pred. No. 1.5e-254; Matches 2360; Conservative 0; Mismatches 5; Indels 384; Gaps 2

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CGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAA
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TGGGGACTTCCTGGTGCGGGAGAGCCAGGGCAAGCAGGAGTACGTGCTGTCGGTGCTGTG			GGGGGGAAGGACCCACGCTGGAGATTCTTAAGAGCCACATTCTCAGGAATTTTCGGCCC	GCCTGCTGCTGCAGGATGACCGCCACTCCACGTCGTGCTCCGGGCCCCGAGGAGCCACCAGAGCCACTCCACGTCGTCCTCGGAGCAGGAGCGAGAGCAGAGCGAGAGCACTCCACGTCGTCGTACGGAGCAGGAGCGAGAGAGA	202 GCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGGCGAGCCCCC	GCAAGTGCTGCAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCCAGGCCAGGCCAGGT 	GCTCCGGAATGAAGAGGAGAACACCCACCCCGGGAGCGGTGCAGCTGCTGGGCAAGAG	GGCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGAGAGAG	GCTGAACGAGCTGACTGTGGAGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAGCT	TGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCCA	н—н (GEAGGATGAGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCGCATCCAGCC	GGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGT 7	CCAGCACCACCAGCTCCTGCTGCCGGCCTGCGGTCACTGCAGGACCTGCACGACACACAC	GAAGCTCTTTGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCA	GGAGGCCAGCAAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTG	482 GCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGTACCA 541
OY 2372 AGGTGCAGCTCCTCAGCGGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCCTGGACTC 2431	Qy 2312 CCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCAGGCCT 2371	OY 2252 GGCCTATGAGCCTGGGCAGCCGACCATCTACCAGGAGCTGCAGAGAGCAT 2311	OY 2192 CCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTG 2251	QY 2132 GGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGG 2191	OY 2072 CTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGG 2131	QY 2012 GGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTA 2071	Qy 1952 GAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGATGGGGTCTATGCAGCCTCAGG 2011	OY 1892 GTGCTGCATCCACCGGGACCTGGCTGGCTGGAACTGCCTGGTGACAGAGAATGTCCT 1951	OY 1832 GAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGAGTACCTGGAGAGCAA 1891	QY 1772 GCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGGCCCGCCTGCGGGT 1831	OY 1712 CAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGA 1771	OY 1652 ACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCCC 1711	QY 1592 CGGACGCCTGCGAGCCGACAACACCCCTGGTGGCGGTGAAGTCTTGTCGAGAGAGA	QY 1532 CCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCGAAGTGTTCAG 1591	QY 1472 CACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGAA 1531	QY 1412 GGAAGGCTTTCCTAGCATTCCTTTGCTCATCGACCACCTACTAGCAGCACCCAGCAGCAGCCCT 1471	Oy 1392

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                                                                                                                                                                           Query Match
Best Local S
Matches 1970
                                                                                                                                                                                                                                                                                          The invention relates to a method for inducing neutralisation of cells or tissues by using a protein binding to CRAM (collapsing response mediator protein-associated molecule) protein or its encoded gene. The proteins and their encoded genes are useful in gene therapy and regenerative medicine, e.g. by inducing neutralisation of mitochondria. They are also applicable in diagnosis, drug development for neural diseases and studying the mechanism of pathosis. The current sequence represents CRAM protein related cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes and proteins participating in neutralization of cells or tissues, useful in gene therapy and regeneration medicine, applicable in discousies, drug development for neural diseases and study of mechanism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; SEQ ID NO 1; 101pp; Japanese
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P-PSDB; ADH43090.
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Query Match Best Local S Matches 856

al Similarity 856; Conser

32.0%; Score 856; DB 1; Lilarity 100.0%; Pred. No. 1.1e-106; Conservative 0; Mismatches 0;

Length 856, Indels

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Sequence 856 BP; 164 A; 265 C; 259 G; 168 T; 0 U; 0 Other;

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25-MAR-2003
27-JAN-1991
                                                  The fur gene, encoding furin, is in the human and cat genomes directly upstream of this fes/fps proto-oncogene sequence. Furin is strongly expressed in specific types of tunours and labelled RNA or DNA probes of the fur gene and antibodies against furin can be used for diagnostic purposes. (See also AAN70061-62 and AAP70056). (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                           Recombinant DNA contg. the fur gene - used for producing and antibodies and as a diagnostic aid in the detection {\sf c}
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P-PSDB; AAP70055.
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                 Osteopathic; antiinflammatory; antirheumatic; antiarthritic; gene therapy; type II collagen; expression; cartilage disease; osteoarthritis; cartilage defect; rheumatoid arthritis; human;
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Matches 606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified protein that promotes type II collagen expression, useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                canine microarray; drug screening; toxicity assay; environmental pollutant; cellular response; gene expression profile; toxic response; liver necrosis; fatty liver disease; protein adduct formation; hepatitis; dog; ds.
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CC environmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in a CC disease state. The sequences are useful as diagnostic agents or markers CC disease state. The sequences are useful as diagnostic agents or markers CC to detect a cellular response in a sample individually or as part of a CC gene expression profile. It is also useful as a target for agents that CC modulate gene expression or activity. The database is useful for CC producing electronic Northerns that allow the user to determine the cell CC type or tissue in which a given gene is expressed and to allow the garticular tissue or cell. The methods are useful for gene in a CC garticular tissue or cell. The methods are useful for determining the CC methods are useful for predicting at least one toxic response or the CC methods are useful for predicting at least one toxic response or the CC gathologies such as those of the liver (liver necrosis, fatty liver CC disease, protein adduct formation or hepatitis), those of the kidney, CC heart, brain or testes, or other pathologies associated with at least one of the toxins. The methods are also useful for predicting or elucidating CC compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin. The present sequence is that of a canine DNA sequence which was claimed for use during the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                significant portion of the canine genome. The isolated canine nucleic acid sequences of the invention may be useful for drug screening and toxicity assays. The invention is therefore useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or
                                                         production of a canine microarray of the invention
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Sequence 527 BP; 97 A; 157 C; 162 G; 98 T; 0 U; 13 Other;

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                          GGGACCCCTTCTCAAGCTGGTGGCCTCTGCAGGC 2369
                                                                                                                                                                                               GCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGGCCGTCTGCCCCTGCCCAGAGCTGT
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GGG-CCCCTTCTCAAGCTGGAGGCCTCTGTGGGC
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                                                       CCAGCTTCNNNNNNNNNNNTACCAGNNGCTGCAGAGCATCCGGAGGCGGCATCGGTGAGGCT
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Pred. No. 1e-41;
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This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a

RESULT 11
ABK84514
ID ABK84
XX
AC ABK84
XX
DT 14-AU

ABK84514 standard;

CDNA; 12263

₽P

ABK84514;

14-AUG-2002

(first entry)

Human cDNA differentially expressed in granulocytic cells #1085.

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CC DNA chip analysis as given in the specification, and comparing the conditions analysis as given in the specification, and comparing the conditating (M2) GA by contacting GC with an agent that alters the conditating (M2) GA by contacting GC with an agent that alters the comparison of at least one gene in Gs; (2) screening (M3) for an agent to capable of modulating GCA or an inflammation (especially chronic) in a cc tissue, an allergic response in a subject expression cc pathogen or sterile inflammatory disease using the gene expression cc pathogen or sterile inflammatory disease, by detecting the level of cexpression in a sample of the tissue of gene(s) from GB, where the level of expression in a sample of the tissue of gene(s) from GB, where the level of expression in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of conflammatory disease, by contactive of inflammation; (4) treating CC (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation of the expression of gene(s) from GB in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M1 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M1 is useful for modulating GCA preferably in an inflammation in tissue; M2 is useful for modulating GCA preferably in an inflammation in a tissue; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M3 is useful for detecting an inflammation condition in a subject to a pathogen or sterile inflammatory disease (e.g. cardiac reperfusion injury, renal reperfusion injury, ARDS, adult conditions, viral infection, parasitic infection, protozoal infection, infection, parasitic infection, protozoal infection,
     Query Match
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                                                                                                                                                                                                                                                                  infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                             Sequence 12263 BP; 2497 A; 3568 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
13.6%;
     Score 362.4;
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                                                                                                             3664 G;
DB 6; Length 12263;
                                                                                                             2534 T; 0 U; 0 Other
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                                                                                                                                                                                                                                                                                                          anti-kinase; ds.
                                                                                                                                                                                                                                                                                                                  Proto-oncogene tyrosine kinase; poTK; tumour; cytostatic; anti-leukemic; gene therapy; protein therapy; vaccine; enzymatic-inhibition; human;
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/*tag= e

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4477. .4573

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Best Local Similarity 99.7
Matches 363; Conservative
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oncogene tyrosine kinase (poTK). The poTK polynucleotides and protein may
be used in the prevention, diagnosis and treatment of diseases associated
with inappropriate poTK expression, such as lung and kidney tumours,
leukemia and stomach adenocarcinoma. poTK may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of poTK by expressing
inactive proteins or to supplement the patients own production of poTK.
The encoded poTK may be used as an antigen in the production of
antibodies against poTK and in assays to identify modulators of poTK
expression and activity. The anti-poTK antibodies and antagonists may be
used to down regulate expression and activity and as diagnostic agents
for detecting the presence of poTK in samples. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15297 BP; 3267 A; 4306 C; 4478 G; 3246 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 3A-G; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding a proto-oncogene tyrosine kinase, useful for the prevention, diagnosis and treatment of e.g. leukemia and lung tumors.
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P-PSDB; ABB07354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents the human poTK genomic DNA sequence
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2547 AAAA 2550
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                                                                                                                                                                                                                                                                                                                                                                                                             GGGGGCCGTCTGCCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG
                                                                                                                                                                                                        GGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCATATGCTGACAGCTCTTTCACAGTCCTG
                                                                                                                                                                                                                                                                                                                                                       TGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG
                                                           CCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGAAACAATAAAACCACTTGTGCCCACTG
                                                                                                            GACTCCTGCCACCAGCATCCACACTGCCGGCAGGATGCAGCGCCGTGTCCTCTGTGTC 1323
                                                                                                                                              GACTCCTGCCACCAGCATCCACACTGCCGGCAGGATGCAGCGCCGTGTCCTCTCTGTGTC
                                                                                                                                                                                     GGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCCTG
                                                                                                                                                                                                                                                            AGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA
                                                                                                                                                                                                                                                                              AGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA
                                                                                                                                                                                                                                                                                                                                    TGCTGGGCCTATGAGCCTGGGCAGCGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG
                                    CCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGAAACAATAAAACCACTTGTGCCCACTG 1329
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/number= 16
12939. .13078
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/number= 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.6%; Score 362.4; DB 6; 99.7%; Pred. No. 3.6e-40; ative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15297;
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intron

/*tag= t /number= 10 9199. .9579 /*tag= u /number= 10

exon

exon

intro

intron

7924. .8007 /*tag= r /number= 9 8008. .9075

number= 9

exon

7485. .7614 /*tag= o /number= 7 7615. .7801 /*tag= p /number= 8 7802. .7923 /*tag= q /number= 8

intron

exon

7159. .7361 /*tag= m /number= 6 7362. .7484 /*tag= n /number= 7 exon

/number= 5 7039. .7158 /*tag= 1 /number= 6

intron

exon

6828. .6965 /*tag= j /number= 5

4887. .6827 /*tag= i /number= 4

number= 4

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9580. .9633 /*tag= v

number= 11

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. .10622

exon

9634. .10229 /*tag= w /number= 11 10230. .10348 /*tag= x /number= 12

exon

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/number= 13
10814 .1093
/*tag= ab
/number= 14
10938 .11176
/*tag= ac

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ARBSULT 13
ABV75414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variation
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2563. .13081
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replace(847,G)
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               /standard name= "Single nucleotide polymorphism"
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/*teg= o
/number= 3
/number= 3
/stag= p
/*tag= p
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3102. .4476
/*tag= m
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replace(2577,C)
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replace(2159,C)
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standard name= "Single nucleotide polymorphism"
776. .2927
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eplace(2484,T)
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eplace(2922,A)
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)28. .3101
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/*tag= v
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7039. 7158
/*tag= w
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7159. 7361
/*tag= x
/number= 6
7362. 7444
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10938. 11176
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6966..7038
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/number= 4
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eplace(5193,G)
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                                                                                                                                                                                                                                                                                                          The invention relates to a newly isolated peptide sequence of a human CC kinase that is related to the proto-oncogene tyrosine kinase subfamily. CC The activity of the kinase of the invention may be described as, CC cytostatic, antiarteriosclerotic, antiinflammatory and antipporiatic. Peptides of the invention are useful in assays to determine the CC biological activity of the protein, in drug screening assays, tissue CC typing and pharmacogenomic analysis. They are also useful in treating or CC diagnosing disorders characterised by an absence of, inappropriate, or CC unwanted expression of the protein, such as inflammation, cancer (e.g. CC leukaemia, lung tumours, kidney tumours or stomach adenocarcinoma), CC arteriosclerosis, and psoriasis. Nucleic acid molecules of the invention CC are useful as probes, primers and chemical intermediates in biological CC assays. The peptide and nucleic acid sequences are useful as models for the development of human therapeutic targets, aid in the identification CC the development of human therapeutic targets, aid in the identification CC therapeutic agence the protein and serve as targets for the development of human chromesome protein of the invention may also be useful in gene therapy. The gene encoding the protein of the invention has been localised to human chromesome 15. The current sequence
                                                                                                                                                                                     Query Match
Best Local Sin
Matches 363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human kinase protein, useful for treating or diagnosing disorders associated with an absence of, inappropriate, or unwanted expression of the protein, e.g. inflammation or cancer, in drug screening assays and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2001; 2001US-00817180.
06-DEC-2001; 2001US-00003295.
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                                                                                                                                                                                                                                                                                              represents the human kinase genomic DNA sequence
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                                        12998
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2307 AGCATCCGAAAGCGGCATCGGTGAGGCTGGGACCCCCTTCTCAAGCTGGTGGCCTCTGCA 2366
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                                      TGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG
                                                                                                             GGGGGCCGTCTGCCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAG
                                                                 TGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAG
                                                                                                                                                                                      Conservative
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/number= 17
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11582. .12938

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11335. .11458
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number= 15
                                                                                                                                                                                                    13.6%;
99.7%;
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                                                                                                                                                                                     Score 362.4; DB 8; Length 15297; Pred. No. 3.6e-40; 0; Mismatches 1; Indels 0;
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RESULT 14
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  exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proto-oncogene tyrosine kinase DNA
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/note= "Single nucleotide polymorphism"
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                                                                                                /note= "Single nucleotide polymorphism'
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/776. .2927
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                                                                                                                                                                                                                                                                                                          /note= "Single nucleotide polymorphism"
replace(2159,c)
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replace(847,g)
/note= "Single nucleotide polymorphism"
1477. .4573
                                                                 note= "Single nucleotide polymorphism"
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[563. .13081
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06-DEC-2001; 2001US-00003295.
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10718.
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eplace(5193,g)
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cag= x
52. .7484
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Query Match 13.6%;
Best Local Similarity 99.7%;
Matches 363; Conservative
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P-PSDB; ADM28581.
Gene encoding type II collagen expression promoting protein, seq
                                           20-MAY-2004
                                                                                      ADL71054;
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                                             (first entry)
                                                                                                                             DNA; 2584
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Pred. No. 3.6e-40;
0; Mismatches 1
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Osteopathic; antiinflammatory; antirheumatic; antiarthritic; gene therapy; type II collagen; expression; cartilage disease; osteoarthritis; cartilage defect; rheumatoid arthritis; human;

gene;

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Best Local Sim
Matches 573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified protein that promotes type II collagen expression, useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis.
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19-APR-2002; 2002US-0373594P
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                 CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCC
                                                                                  GGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGC
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CTGGTAGGTGAAAATAATGTTCTGAAAATCAGTGACTTTGGAATGTCTCGTCAAGAGGAT
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pred. No. 1.3e-35;
0; Mismatches 342;
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CTTCAGAAAGAGCTCACTATCATC
                         ATCTACCAGGAGCTGCAGAGCATC 2312
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                                                        TCCAAAATCATGATGAAGTGTTGGGATTATAAACCTGAAAATCGCCCTAAGTTCAGTGAA
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Search completed: March 19, 2005, 04:31:15 Job time: 1290.71 secs

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Listing first 45 summaries
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7.4	7.4	7.5	8.3	8.3	8.6	10.0	10.0	10.2	10.2	10.2	10.3	11.1	11.1	11.9	12.3	œ	O	o	13.6	13.6	13.6	13.6	14.0	14.0	14.1
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CQ776660 Sequence	AX481387 Sequence	Z27409 H.sapiens m	E01406 DNA sequenc	A06936 H.sapiens f	CQ726604 Sequence	X52844 Drosophila	US0450 Drosophila	BT003462 Drosophil	CQ591168 Sequence	CQ597087 Sequence	AB006567 Ephydatia	AR236724 Sequence	AR175607 Sequence	Y17051 Sycon rapha	J03358 Human tyros	AF187884 Canis fam	AC004586 Homo sapi	AC124248 Homo sapi	AC003004 Human Chr	AR456324 Sequence	AR183262 Sequence	X06292 Human c-fes	X13412 Rat mRNA fo	M32054 Mouse tyros	U76762 Mus musculu

ALIGNMENTS

8	B &		Dh 1	S S	Db	Qy	Вb	Q	Query Match Best Local Matches 267	ORIGIN	source	JOURNAL FEATURES	BTITI	AUTHORS	REFERENCE	ORGANISM	SOURCE	VERSION	DEFINITION	RESULT 1 AR183261
241 GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG	GGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTG	TERMENTANCIA CITARCALA CITA TERMENTA CENTRA CENTRA CON CATERCA CON CONTRA CARRACA CATERCA CONTRA CARRACA CATERCA CONTRA CATERCA CONTRA CATERCA	121 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGGCATGAGAAAGTGGATGGCCCAGC 180	121 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGC 180	61 GGAACAGCACTATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGC 120	61 GGAACAGCACTATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCCACGGGTCCTGC 120	1 TCCGGGGTCCGCACCGGGCCTGAGTCCGAGGCCGTCCCCAGGAGCAGCAGCTGCCCCGTGC 60	1 TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCCGTCCCAGGAGCAGCTGCCCGTGC 60	/ Match 100.0%; Score 2674; DB 6; Length 2674; Local Similarity 100.0%; Pred. No. 0; 1es 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/moi_type="unassigned DNA"	/organism="unknown"	22-JAN-2	human kinase proteins, and uses thereof	Di Francesco, V. and Beasley, E.M.	es 1 to 2674)	Unknown.	Unknown.	AR183261 AR183261.1 GI:20226854	Sequence 1 from patent US 6340584.	262 1 112 112 122

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TGCAGGCCAGGAGTTGCTGCAGACCAAGCCTGAGCACCTGGGGCCGGGGAGCCCCCTGCGCCAGGAGCTGCAGGAGCCCCCCCAGGAGCAGGAGCCCCCCAGGAGCAGGAGCAGGAGCCAGAGCCAGGAGCAGAGCGAGCTGGTCGTCCTCGAGGAGCAGGAGCGAGC	AGCTGCTGGGCAAGA	AGCCTGGGGAGCTCC AGCTGCTGGGGAGCTCC AGTGCTGGCAGAGAGCCC AGTGCTGGAGAGAGCCCCCAGTGACAGAGCAGATGACCAGGCTGCAACAGG	ANGATTAGCACCTGG	ATGTGCGCAGCCTGT	TCCTGGGCTGAGATCA GAGGATCTGAACTCAG [
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OY 421 GCGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGGCAGG	OY 361 GGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACA 420	QY 301 CCAGCCAAACTGAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAG 360	QY 241 GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG	OY 181 GGGTCAAGAGTGACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTG 240	QY 121 AGCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGC 180	OY 61 GGAACAGCACTATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGC 120	OY 1 TCCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCCGTCCCAGGAGCAGCTGCCCGTGC 60	Query Match 100.0%; Score 2674; DB 6; Length 2674; Best Local Similarity 100.0%; Pred. No. 0; Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	gour RIGIN	TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof JOURNAL Patent: US 666187-A 1 03-FEB-2004; FEATURES Location/Ouglifiers	NISM Unknown. Unclassified. 1 (bases 1 to 2674) DRS Gan W. Ye.T. Di Francesco V.	GI:4					2461 ANCAATAAAACCACTTGTGCCCACTGAAAAAAAAAAAAAA	Oy 2461 ATGCAGCGCCGTGTCCTCTGTGTCCCTGCTGCTGCCAGGGCTTCCTCTTCCGGGCAGA 2520
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BC035357.1
                                                                                                                                                             Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: e Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 133769
                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
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Submitted (31-JUL-2002) National Institutes of Health, Mammalian Submitted (ollection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens feline sarcoma oncogene, mRNA linear PRI 29-JUN-20
HOMO SAPIENS feline sarcoma oncogene, mRNA (cDNA clone MGC:34142
HMAGE:5170548), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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12477932
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/organism="Homo Bapiens"
/mol_type="mRNA"
/mbl_type="mRNA"
/db xrefe="taxon:9606"
/clone="MGC:34142 IMAGE:5170548"
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Query Match 88.1%;
Best Local Similarity 92.5%;
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GCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCCAAGCGCAAGTACCA
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                                                                                                                               GCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAG
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CVTFDESLLEEGEPLEPGELQINELTVESVQHTLTSVTDELAVATEMVERRQENVTQL
QQELRNEEENTHPRER VQLLGKRQVLQEALQGLQVALCAAARIQAQQELLQTKLEHLG
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PGEPPVLLLQDDRHSTSSSEGEREGRTTPLEILKSHISGIFRFKFSLPPLOLIPE
PGEPPVLLLQDDRHSTSSSEGEREGRTTPLEILKSHISGIFRFKFSLPPLOLIPE
VQKPLHEQLWYHGAIPRAEVAELLVHSGDFLVRESQGKQEYVLSVLWDGLPRHFIIQS
LDNLYRLEGEGFPSIPLLIDHLLSTQQFLTKKSGVVLHRAVFKKWVLNHEDLVLGEQ
IGRGNFGEVFSGRLRADNTLVAVKCRETLPDDLKAKFLQHARILKQVSHPNIVTLIG
VCTQKQPIYIVMELVQAGDFLTFLRTEGARLRVKTLLQWVGDAAAGMEYLESKCCIHR
DLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPKWTAPEALNYGRYSSE
SDWSFGILLWETTSLGASFYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQCWA
VEDCONESEETTYPCTGCTSVATUS
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/product="V-FES feline sarcoma viral/V-FPS fujinami avian sarcoma viral oncogene homolog"
/protein_id="AAH35557.1"
/db_xref="GI:23271525"
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ON X52192.1 GI:29890

ADS fee cellular oncogene.

CE Homo sapiens (human)

KGANISM Homo sapiens (human)

EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 2771)

Alcalay, M., Antolini, F., Van de Ven, W.J., Lanfrancone, L.,

Grignani, F. and Pelicci, P.G.

Characterization of the 5' end of the gene

Oncogene 5 (3), 267-275 (1990)
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122 GCAMATCEAGGACCCGACCTTCOTCTACTGAGGACTAGGAAAAGTCGATTCCCCCACCCGC 181 123 GCTCHAGACTGACAGGACTTCCTTCACTGAGGACATTCCCCCCACCTGAGGACATTCCCCCACCCGC 182 124 GCTCHAGACTGACAGGACTTCCTCACCCACCTCCCCCCCCCC
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Query Match Best Local Similarity 92.3%; Pred. No. 0; Best Local Similarity 92.3%; Pred. No. 0; Matches 2558; Conservative 0; Mismatches 1; Indels 211; Gaps 2; Qy 2 CCGGGGTCCGCACCGGGCCTGAGTCGGTCCGAGGCCGTCCCAGGAGCAGCTGCCCGTGCG 61	AUTHORS Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J., Mikita,T. and Tai,J. TITLE Genes expressed in foam cell differentiation JOURNAL Patent: WO 017739-A 256 18-OCT-2001; Incyte Genomics, Inc. (US) FEATURES Location/Qualifiers Source /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="lncyte ID No: 997347.6" ORIGIN	RESULT 5 AX281847 LOCUS LOCUS AZ281847 AX281847 AX281847 AZ281847 AZERINITION Sequence 256 from Patent WOO177389. ACCESSION AX281847 VERSION AX281847 VERSION AX281847 AX281847 LOTUS ORGANISM Homo sapiens (human) CORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Oy 2432 CTGCCACCAGGATCCACACTGCCGGCAGATGCAGGCCGTGTCCTCTCTCT	2312 CCGAAAGCGGCATCGGTGAGGCTGGGAGCCCCCTTCTCAAGCTGGTGGCCTCTGCAAGCCTCTCAAGCTGGTGGCCTCTGCAAGCCTCTCAAGCTGGTGGCCTCTGCAAGCCTCTCAAGCTGGTGGCCTCTGCAAGCCTCTTGCAAGCTGGTAAGCTGGCAAGCCTCTTGCAAGCTTGCAAGCCTCTTCAAGCTGGTGGCCTCTTGCAAGCCTCTTCACAGTCCTTGACACCTCTCAAGCTGCTATATGCTGACAGCTCTTCACAGTCCTTGACTCCTGAACTCTTAACTCCTGAAGCTGCTTGACTCCTTGACTCCTTGACTCCTTGACTCCTGAGCTCCTTGAAGCTCTTGAAGCTCTTGAAGCTCTTGAAGCTCTTGAACTCCTTGAAGCTCTTGAAGAAGAAGAAGAAGAAGAAGAAAAAAAA	Db 2286 CTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGGGAGACCTTCAGCCTGGG 2345 Qy 2132 GGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGAACACGGAGGTTTGTGGAAGAGGGGG 2191
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1021 TGGCTGTGGCCACCGAATGGTTCAGGCGGCAGGAGATGGTTACGCAGCGCAGCACAGG 1080	841 CTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCT 900	661 ACCAGCACCACCACCACCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACG 720	481 AGCTGAAGAGCCAGTACCGAGCTCTTGGCACGGGACAGTGCCCAAGCCAAGTACC	361 GGCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAAGCGCAGCAGCAGAGACCTACA 420	

2130 2457	071 ACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGC
2070 2397	ω o
2010 2337	951 TGAAGATCAGTGACTTTG
1950 2277	891 AGTGCTGCATCCACCGGGACCTGGCTGGCTGGACACGAGAGAAGAATGTCC
1890 2217	831 TGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCA
1830 2157	771 AGCTTGTGCAC
1770 2097	711 CCAACATCGTGCG 038 CCAACATCGTGCG
1710 2037	651 CACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGA
1650 1977	91 GCGGACGCCTGCGAGCCGACAACACCCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCC
1590 1917	531 ACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCGAAGTGTTCA
1530 1857	471 TCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTG
1470 1797	411 GGGAAGGCTTTCCTAGCATTCCTTTGCTCATCGACCACCTACTGAGCACCCAGCAGCCCC
1410 1737	392ACCTGTA
Ö	618 CTGGGGACTTCCTGGTGCGGGAGAGCCAGGGCAAGCAGGAGTACGTGCTGTCGGTGCTG
1391	392
1617	558 AGCAGCTGTGGTACCACGGGGCCATCCCGAGGGCAGAGGTGGCTGAGCTGCTGGTGCAC
1391	392
1391 1557	381 CCAAGTTCTCG
1380 1497	321 AGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTT
1320 1437	261 CGCCTGTGCTGCTCCTGCAGGATGACCGC
1377	318 TGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCC

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182 GGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGG
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                                                                                                      62 GAACAGCACTATIGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCA
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 11154 from Patent WOO2068579.
CQ725220 CQ725220.1 GI:42286077
                                                                                                                                                                                                                                                                                                      Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                   GCAAATGCAGGAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCG
                                                                                       GAACAGCACTATGGGCTTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGTCCTGCA
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/mol_type="unassigned DNA"
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1021 GCTCCGGAATGAAGAGAACACCCACCCCGGGAGCGGTGCAGCTGCGGCAAGAG 1080 1142 GCAAGTGCTGCAAGAAGACACCCCACGCGGAGCGGTGCAGCTGCGGCCAAGACT 1201	2 GCTGAACGACTGACTGACTGAGAGAGCGTGAGCACACGCTGACCTCAGTGACGAGATGAGCT 10	842 TGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTG 901	722 GGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGT 781	602 GAAGCTCTTTGCTCACCACACCGCTATGTGCTGGCGTGCGGGCTGCGCAGCTACACCA 661	482 GCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGTACCA 541	362 GCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGCAGCAGCAGCAGCAAGACCTACAG 421	1 GGTCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGG 1 2 GGGCCAGAGCCGGGCCATCAGCCCCTGACACCCCATCAGTCAG
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2012 GGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTA 2071		1812 GAAGACTCTGCCGGGAGATGGTGGGGGATGCAGCCAGCATGGAGTACCTGGAGAGCAA 1891	1712 CHACCECCUCTOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	1621 CACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGTCCAG 1680 1532 CCATGAGGACCTGGTGTTGGGTGACAGATTGGACGGGGAAGTTTGGCCGAAGTGTTTCAG 1591	1501 GGATGGTCTGCCCCGGCACTTCATCATCCAGTCCTTGGATAACCTGTACCGACTGGAAGG 1560 1412 GGAAGGCTTTCCTAGCATTCCTTTGCTCATCCACCACCTACTGAGCACCCAGCAGCCCCT 1471	GCAGCTGTGGTACCACGGGGCCATCCCGAGGGCAGA TGGGGACTTCCTGGTGCGGGAGAGCCAGGCCAAGCA	1322 GGGGGGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCC 1381

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Wilks,A.F. and Kurban,R.R.
Isolation and Structural analysis of murine c-fes cDNA clones Oncogene 3 (3), 289-294 (1988)
89083198
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Mouse c-fes proto-oncogene mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (house mouse)
                                                  SVIIRERHSIRKTYNEQWQQIQQELTKTHSQDIEKLKTQYRTIVRDSTQARRKYQEAS
KOKDROKAKDKYVRSLWKLFAHHRYYLGVRAAQLHHHHHRYMLPGLLQSLQDLHEB
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KPLYEQLWYHGAIPWAEVAELLTHTGDFLURESQGKQEYVLSVWMDGHPRHFIIQSLD
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RGNFGEVFSGRLRADNTPVAVKSCRETLEPDLKAKFLDAAAILKQYNHPNIVRLIGVC
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VWSFGILLWETFFSLGASBPYPNITNOQTREFVEKGHRLPCPELCPDAVFRLMEQCWAYE
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/db_xref="G1:50956"
/db_xref="G0:50956"
/db_xref="G0:50956"
/db_xref="UniProt/Swiss-Prot:P16879"
/db_xref="UniProt/Swiss-Prot:P16879"
/translation="MGFSSELCSPQGHGAVQQMQEAELRLLEGMRKWMAQRVKSDREY
AGLLHHMSLQDSGGQSWSSGPDSPVSQSWAEITSQTENLSRVLRQHAEDLNSGPLSKL
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/mol_type="mRNA"
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one_lib="lambda gt1:
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                                                                                                                                                                                                             TGTGTCACGTTCGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTTGGGGAGCTC
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   GAGCTCCGGAATGAAGAGGAGAACACCCCACCCCCGGGAGCGGGTGCAGCTGCTGGGCAAG 1139
                                                             CTGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAG
                                                                                                                                      CAGCTGAACGAGCTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAG
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                                        CAGCTGAATGAGTTGACCTTGGAGAGCGTGCAACACACGCTGACTTCTGTGACAGATGAA 1007
                                                                                                                                                                                        TGTGTCACTTTTGATGAGTCGCTTCTTGAAGACGGGGAACAGCTGGAGCCAGGGGAGCTG
                                                                                                                                                                                                                                                              CCTGAGTTTGAGTACCTAGGCTTCCTGCGACAATATGGATCCACCCCTGATGTGCCACCT
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1079

Ū	2009	1950 CTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGGAAGCCGATGGGGTCTATGCAGCCTCA	
	1949 2141	1890 AAGTGCTGCATCCACCGGGACCTGGCTGCTGGAACTGCCTGGTGACAGAGAAGAATGTC	
, ,	1889 2081	830 GTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCATGGAGTACCTGGJ 	
	1829 2021	70 GAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGGCCCGCCTGCGG	
	1769 1961	710 CCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATG	
	1709 1901	650 CCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCAC	
	1649 1841		
	1589 1781	530 AACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCGAAGTGTTC	
	1529 1721		
	1469 1661		
, -	1409 1601		
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	1379 1361		
	1319 1301	60 CCGCCTGTGCTGCTGCTGCAGGATGACCGCCACTCCACGTCGTCCTCCGAGCAGGAGCGA	
	1259 1247	200 CTGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCCTGGGCCCCGGCGAGCCCC	
	1199 1187	140 AGGCAAGTGCTGCAAGAAGCACTGCAGGGCTGCAGGTAGCGCTGTGCAGGCCAGGCCAAG	
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Pujinami sarcoma virus

Pujinami sarcoma virus

Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.

1 (bases 1 to 2715)

Chen, L.H., Hatada, B., Wheatley, W. and Lee, W.H.

RS Chen, L.H., Hatada, B., Wheatley, W. and Lee, W.H.

RS Chen to 2715)

Single amino acid substitution, from Glu1025 to Asp, of the fps oncogenic protein causes temperature sensitivity in transformation and kinase activity

AL Virology 155 (1), 106-119 (1986)

RE 87044080

ED 2877522

Original source text: Fujinami sarcoma integrated viral DNA, clone
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                / COUNTY OF THE TOTAL OF THE TO
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/mol_type="genomic RNA"
/db xref="taxon:11885"
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PVKWTAPEALNYGWYSSESDVWSFGILLWEAFSLGAVPYANLSNQQTREAIEQGVRLE
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1012 CAGATGAGCTGGCCTGTGGCCACCGAGATGGTGTTCAGGCGGCAGGAGAGTGGTTACGCAGC 1071	GGGAGCTGCAGCTGAATGAGCTGACCATCGAGAGCGTGCAGCACTCCCTGACATCGATTG		892 TCCCACCCTGTGTCACGTTCGATGAGTCACTGCTTGAGGAGGTGAACCGCTGGAGCCTG 951	832 GCATCCAGCCTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGGGTCCGCCACCTGACG 891	772 GCAGCTGCTGCAGGATGAGGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCC 831	GCTGCAGCAGAGATGGTCCTTGTTTTGAAGGAGATTCTTGGGGAGTACTGTAGCATCA	12 ACCTGCACGAGGAGATGCCTTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTA	652 AGCTACACCACCAGCACCAGCTCCTGCTGCCCGGCCTGCTGCGGTCACTGCAGG 711	755 GCAGCCTGTCGAAGCTCTATGCCTTGCACAACCAGTACGTGCTGGCTG	95 GCAAGTACCAGGAGGCCAGCAAAGGACAAGGAGGAAAAAGGCGAAGGAAAAATACGTGC	532 GCAAGTACCAGGAGGCCAAGCAAGACAAGGACCGTGACGAAGGACAAGGACAAGTATGTGC 591	472 ACATTGAGAAGCTGAAGAGCCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGC 531	575 AGGTCTTCAGTGAGCAGCAGCTCAGCCAGGAGTACGCCTGGACCACACACA	AGACCTACAGCGAGCAGTGGCAGCAGCAGCAGGAGCTCACCAAGACCCCAGCCAG	352 TGAACTCAGGGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTAGCCA 411	455 GGGTTCTGGCAAGCCAGACTGAGACACTGAGCCAGACGCTGCGGCGGCACGCGGAGGAGG 514	292 CTGAGATCACCAGCCAAACTGAGGGCCTGAGGCGCTTGCTGCGGCAGCACCACGCAGAGGATC 351	232 AGGACAGTGGGGGCAGAGCCGGGCCATCAGCCCCTGACAGTCAGT	335 CCAAGAGCGACCGGGATACGCGGGGATGCTACCACATGTTCTCTCTAGCTGGAGAAAC 394	TCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGC	GCTGCAGGACAGCGAGTTGCGCCTCCTGGAGCTGAAGAAGTGGATGTCACAGCGTG	63	64 ACAGCACTÁTGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGC 123	Query Match 38.3%; Score 1024.8; DB 14; Length 2715; Best Local Similarity 66.3%; Pred. No. 3.9e-147; Matches 1650; Conservative 0; Mismatches 612; Indels 228; Gaps 3;	EEEGCEBUYIKUMBIUEHKKESEGAYHQUULALKKKHK"	יייייייייייייייייייייייייייייייייייייי
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                                                                                                                                                                                                                                                                                                                                  2 (bases 1832 to 1881; 2851 to 2902)
Carlberg.K., Chamberlin,M.E. and Beemon,K.
The avian sarcoma virus PRCII lacks 1020 nu
transforming gene
Virology 135 (1), 157-167 (1984)
84225820
                                                                                                                                                                          sarcoma virus (FSV) transforming protein p130, the product of gag-fps fused gene. p130 is highly homologous to the gag-fes sequence of feline sarcoma virus (see separate entries), and is homologous in the 280 residue carboxyl end (including the phosphoacceptor tyrosine residue) of Rous sarcoma virus p60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibuya, M. and Hanafusa, H.
Nucleotide sequence of Fujinami sarcoma virus: evolutionary relationship of its transforming gene with transforming gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujinami sarcoma virus
J02194 K01827 K01828
J02194.1 GI:209686
                                                                                                                                                                                                                                                              Original source text: FSV (Fujinami sarcoma virus), unintegrated circular DNA [1],[2].
The sequence of 1182 amino acids was deduced from the Fujinami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujinami sarcoma virus
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c-myc proto-oncogene; complete
Fujinami sarcoma virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sarcoma viruses
                /note="5' LTR"
247. .267
                                                                /organism="Fujinami sarcoma virus"
/mol_type="genomic RNA"
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1550. .4171
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/translation="Meavikvissacktycgktspskkeigamlsqlqkegilmslsd"
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arireelasgapppyvgsglaypslawgpopperaepertistgraactur
almssplephdyntnpmrvilgpaphalmdamasgolherpopgetystsactur
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goraksdreyagmlhhdfsqlekqegtgelkarphssqleswylasgotelkcyrslv
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rdvrbuysgrssdywsfgillmersgrandntypyavsgrandegevgrandegerpegcp
EDVYRLMQRCWEYDPHRRPSFGAVHQDLIAIRKRHR"
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1392	
RESULT 10 AF033810 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	8
AF033810 4788 bp RNA linear VRL 03-DEC-1998 ON Fujinami sarcoma virus, complete genome. N AF033810.1 GI:2801466 Fujinami sarcoma virus Fujinami sarcoma virus Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.	1462 AGCITGAMAGACATTGCCCACCACCACCTGCTCACCAACCACCTGCTGCAAAAACCCTTCCACCAAAAACCCTTCCCACCAAAAACCCTTCCCACCA

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Chappey,C.
Direct Submission
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Cold Spring Harbor Labo
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Petropoulos, C.J.
Appendix 2: Retroviral taxonomy,
genetic maps
                     TCAAGAGTGACAGGGAGTATGCAGGACTGCTTCACCACATGTCC-----CTGC
                                                                    GGCTGCAGGACAGCGAGTTGCGCCTCCTGGAGCTGATGAAGAAGTGGATGTCACAGCGTG
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llarity 66.3%;
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LPTLHESLYSLQQEMVLVLKEILGEYCSITSLVQEDVLAHIGKVAHAVENIDPATEYS
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PEALMYGWSSESDVWSFGILLMEAFSLGAVPYANLSNQQTREALEQGVRLEPPEQCP
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4196. .444
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899. .1087
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| 085. .1309
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                                           GCGAGCCCCGCCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGC
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	82 AGAAGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGG	
18	122 TCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACACAGGGAGTTTGTGGG	
2121 3719	2062 ACGGCCGCTACTCCCTAAAGCGACGTGTGGAGCTTTTGGCATCTTGCTCTTGGGAGACCT :	
2061 3659	2002 CAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACT:	
2001 3599	1942 AGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGATGGGGTCTATG:	
1941 3539	1882 TGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGGCTG	
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1821 3419	1762 TCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGCCC:	
1761 3359	1702 ACAGCCACACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACA:	
1701 3299	1642 AGACGCTCCCACCTGACGTCAAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGT	
1641 3239	1582 AAGTGTTCAGCGGACGCCTGCGAGACCAACACCCTGGTGGCGGTGAAGTCTTGTCGAG	
1581 3179	1522 GGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGGAGATTGGACGGGGGGAACTTTTGGCG :	
1521 3119	1462 AGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGT	
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1391 2879	2820 CGCTGTGCCAGCAGGCCTGGTACCACGGGGCCATCCCGCGCTCGGAGGTGCAGGAGCTGC	
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2759 1391	CTGCGCTGAAGACCATCAAGAACCACATCTCGGGCA	
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1 (bases 1 to 856)
1 (bases 1 to 856)
Van de Ven.W.J.M., Roebroek, A.J.M. and Schalken, J.A.
Van de Ven.W.J.M., mRNA, protein, antibodies, and a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of detecting tumor cells
Patent: BP 0246709-A 2 25-NOV-1987;
Stichting Katholieke Universiteit
Location/Qualifiers
GGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGGGACTTCCTGACCTTCCTCCGCACGG
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                                                                                                                                           TGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCCGAGAGGGAAGCCGATG 1992
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/tdb_xref="G1:4526613"
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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2954 TCCCGGGAGGAAGCCGATGGGATCTACGCGGCCTCAGGGGGCCTCAGACTAGTTCCGGTG	TIGOTGCAAGAAGCACTG 1163	1104 ACCCACCCCGGGAGCGGTIGCAGCTTGGTGAGAAGCAGTGCTIGCAAGAAGCACTGCTIGGTGAAGAGGAGAGG	B &
1974 TCCCGAGAGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGGCCTCA			Matc
1914 GCTGCTCGGAACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATG	h 4901;	32.0%; Score 854.4; DB 13; imilarity 77.7%; Pred. No. 4.7e-121;	Quer
1854 GGGGATGCAGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTG			ORIGIN
1794 CTGACCTTCCTCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTG	. `	88129048 8829460 Location/Qualifie	MEDLINE PUBMED FEATURES
1734 GTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGG	en feli	Kemp, A.W., Bloemers, H.P. and Van de Ven, W. Structural analysis of a variant clone of sarcoma virus Virus Res. 8 (4). 349-361 (1987)	TITLE
1674 CTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGT	Verbeek J.S. van der	<pre>d unclassified Unclassified. 1 (bases I to 4901) Van Groningen J J Van den Onweland A M</pre>	ORGANISH
1614 ACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTT		M22820 M22820.1	ACCESSION VERSION KEYWORDS
1554 GAGCAGATTGGACGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAAC	linear UNA 04-AUG-1993 al DNA of the variant	M22820 M22820 M22820 Figure 4. Nucleotide sequence of the provin	M22820 LOCUS DEFINITION
1494 CTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGT	_	841 ACTIGIGCCCACTGAA 856	D d d
1434 TTGCTCATCGACCACCTACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTC	3GCAGAAACAATAAAACC 840	781 GTCCTCTGTGTCCCTGCTGCTGCCAGGGCTTCCTCTCCGGGCAGAAACAATAAAACC 2533 ACTTGTGCCCACTGAA 2548	& B
1392ARCCIGIRCGACIGGAGGGGAAGGCTIICCIAGCAITCE	36CAGGATGCAGCGCCGT 780 3GCAGAAACAATAAAACC 2532	721 TCTTCACAGTCCTGGACTCCTGCCACCAGCATCCACACTGCCGGCAGGAGGATGCAGCGCCGT 2473 GTCCTCTGTGTCCCTGCTGCCTGCCAGGGCTTCCTCTTCCGGGCAGAAACAATAAAACC	Q G
4. (2 4	2413 TCTTCACAGTCCTGGACTCCTGCCACCAGCATCCACACTGCCGGCAGGATGCAGCGCCGT	. 6
1392	AGCTCATATGCTGACAGC 2412	2353 TIGGTGGCCTCTGCAGGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCATATGCTGACAGC	B 5
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2174 CTGCAGCTCGTACCAGAGGTGCAGAAGCCCCTGCACGAGCAGCTGTGGTACCACGGGGCC	GGACCCCCTTCTCAAGC 2352	2293 ACCAGGAGCTGCAGAGCGCATCCGAAAGCGGCATCGGTGAGGCTGA	Ş
2		541 GGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGCCCAGCTTCAGCACCATCT	당 .
1344 GAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTCG	TCCTGATGCCGTGTTCA 540 CAGCTTCAGCACCATCT 2292	481 AGTTTGTGGAGAAGGGGGGCCGTCTGCCCTGCCCAGAGCTGTG	영 문
2054 GACCGCCACTCCACGTCCTCCTCGGAGCAGAGCGAGAAGGGGGAAGGACACCCACC	FICCTGATGCCGTGTTCA 2232	2173 AGTTTGTGGAGAAGGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCTCCTGATGCCGTGTTCA	Ş
1994 CANGUCCANGUTGGANGCAGUTGGGCUCUCGGCGANGLULUUGUCUCGACGAGAAGGGGGGAAA	JCAATCAGCAGACACGGG 2172	2113 GGGAGACCTTCAGCCTGGGGGCCTCCCCTATCCCAACCTCAGCAATCAGCAGACACAGGGC 111	유 성
1224 CAGACCAAGCTGGAGCACCTGGGGCCCCGGCGAGCCCCGGCTGTGCTGCTGCAGGAT			망
1164 CAGGGGCTGCAGGTAGCGCTGTGCAGCCAGGCCAAGCTGCAGGACGAGGAGTTGCTG	AGTGGACCGCACCTGAGG 360	301 GGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGG 2053 CCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGGGGCTTTGGCATCTTGCTCT	5 B

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                                                                                                                                                                                                                                                                                                                     the transforming polyprotein of the snyder-theilen strain of feline sarcoma virus (fesv) include the transforming gene (fes) product with tyrosine specific protein kinase activity. the encoded protein sequence was compared with the gene products of gardner-arnstein (ga) strain (see fesvgaonc), fps gene of avian fujinami sarcoma virus (see fev), and src gene of avian sarcoma virus, the reported sequence contains a 145bp deletion against the ga strain, and the authors argue that they sequenced a defective clone, the missing nucleotides are denoted by n's (see fesvgaonc between 1818 and 1964 for presumed base sequence), the last 24 bases represent the sequence of feline leukemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peline Barcoma virus
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Viruses; Retroviridae; Mammalian type C
retroviruses; 1-Mammalian type C virus group.
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1 (coloridae sequences of feline retroviral oncogenes (v-fes) provide evidence for a family of tyrosine-specific protein kinase genes coll 30 (3), 775-785 (1982)
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PEKPFTLPQPLSPQPSAPLYSSLYRERENPAEESQALPLREGENNRPQYWPFSASDLY
PGGHGPPPSGPRTPAASPIVSLURERENPAEESQALPLREGENNRPQYWPFSASDLY
organism="Feline sarcoma virus"
|mol_type="genomic RNA"
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/strain="snyder-theilen"
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Query Match Best Local S Matches 1147	#atch 31.5%; Score 842.2; DB 14; Length 2397; scal Similarity 76.9%; Pred. No. 3.4e-119; s 1147; Conservative 0; Mismatches 134; Indels 211; Gaps 2;	
3	1104 ACCCACCCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCTGCTAGAAGAAGAAGCACTG 1163	
ŏ	889 ACCCACCCCGGGAGCAGGTGCAGCTGCCAAGAAGCAGGTGTTGCAAGAGGCGCCTG 948	
ਝ	1164 CAGGGGCTGCAGGTAGCGCTGTGCAGGCCAAGGTGCAGGACCAGGAGGTTGCTG 1223	
ŏ	949 CAGGCGCTGCAGGTGGCGTTGTGCAGCCAGGCCCAGGCGGAGCTGCTG 1008	
उ	1224 CAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCCCGCCTGTGCTGCTCCTGCAGGAT 1283	
ŏ	1009 CAGGCCAAGCTGGAGCAGCTGGGCCCCGGAGCCCCGCCCG	
₹	1284 GACCGCCACTCCACGTCCTCCGCAGGAGCAGGAGGGGGGGG	
ŭ	1069 GACCGCCACTCCACGTCCTCGGAGCAGGAGCGAGAAGGGGGAAGGACACCCACC	
3	1344 GAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTCGGAACCTGTACCGA 1403	
ਰੱ	1129 GAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTCGCTCCCTCC	
₹	1404 CTGGA 1408	
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ቻ	1249 CTCCCACGGCAGAGGTGGCTNNNNNNNNNNNNNNNNNNNN	
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₹	1409AGGGGAAGGCTTTCCTAGCATTCCT 1433	
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¥	1434 TTGCTCATCGACCACCTACTGAGCACCCAGCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTC 1493	
ਲੋ	1429 TTGCTCGTCGACCACCTGCCTGCGCTCCCAGCAGCCCCTCACCAAGAAGAGCGGTATTGTC 1488	
Ÿ	1494 CTGCACAGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGT 1553	
ਲੋ	1489 CTCAACAGGGCTGTGCCCAAGGACAAGTGGGTGCTAAACCACGAGGACCTGGTGTTGGGT 1548	
¥	1554 GAGCAGATTGGACGGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAAC 1613	
ਲੋ	1549 GAGCAGATCGGGCGGGGAACTTTGGAGAAGTGTTCAGTGGACGCCCTGAGGGCCGACAAC 1608	
ই	1614 ACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTT 1673	
ਲੋ	1609 ACTCTAGTGGCCGTGAAATCTTGTCGCGAGACACTCCCCACCTGACATCAAGGCCAAGTTT 1668	

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Gardner-Arnstein feline leukemia oncovirus B
Gardner-Arnstein feline leukemia oncovirus B
Gardner-Arnstein feline leukemia oncovirus B
Viruses; Retroid viruses; Retroviridae; Mammalian type C
retroviruses; 1-Mammalian type C virus group.
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1 (bases 1 to 2946)
1 Wucleotide sequences of feline retroviral oncogenes (v-fes) provide evidence for a family of tyrosine-specific protein kinase genes cell 30 (3), 775-785 (1982)
the transforming polyprotein of the gardner-arnstein strain of feline sarcoma virus (fesv) include the transforming gene (fes) product with tyrosine specific protein kinase activity. the enc protein sequence was compared with the gene products of
                                                                           strain.
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Local Similarity
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sarcoma virus (see fsv), and src gene of avian sarcoma virus. the
last 24 bases represent the sequence of feline leukemia virus.
Location/Qualifiers
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/protein_id="AAA43041.1"
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| mol_type="genomic RNA"
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Pred. No. 1.6e-117;
0; Mismatches 198;
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                                                                                 Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 4788)
Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W. and Kichardson, P.
                                                                                                                                                                                                                                                                     BC073445

Xenopus laevis MGC80946 protein, IMAGE:5516233), complete cds.
Dev. Dyn. 225 (4), 384-391 (2002)
12454917
2 (bases 1 to 4788)
                                                                 Genetic and genomic tools
                                                                                                                                                                                                                                       BC073445.1
                                                   initiative
                                                                                                                                                                                                     Kenopus laevis (African clawed
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AUTHORS
TITLE
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PUBMED
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                                                                                                                                                    gene
                                                                                                    SdC
                                                                                                                                                                                                                                                                                                        Bource
                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 155 Row: j Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development, 610
20892-7510, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   info@bcgsc.bc.ca
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399. .2867
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                                                                                   /gene="MGC80946"
                                                                                                                                    /gene="MGC80946"
                                                                                                                                                                note="Vector: pCMV-SPORT6"
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31/32, Xenopus"

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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Mazra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
P. 12477932
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chou Sier Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angellque Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Conso
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission

Submitted (14-JUN-2004) National Institutes of Health, Xenopus Gene Submitted (XGC), National Institute of Child Health and Human Collection (XGC), National Institute of Commandation (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project
Contact: XGC help desk
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Klein, S. and Gerhard, D.
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Best Local Similarity
Matches 1426; Conserv
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Pred. No. 3e-91;
0; Mismatches 834;
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Sequence 2, Appli
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Sequence 69, Appl
Sequence 30, Appl
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ALIGNMENTS

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Sequence 2, Application US/10003295
[Sequence 2, Application No. US20020168741A1]
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[TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
[TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
[TITLE OF INVENTION: THEREOF
[FILE REFERENCE: CL001183DIV
[CURRENT APPLICATION NUMBER: US/10/003,295
[CURRENT APPLICATION NUMBER: 2001-12-06
[NUMBER OF SEQ ID NOS: 4
[SOFTWARE: FRASTSEQ for Windows Version 4.0
[SEQ ID NO 2
[LENGTH: 752
[TYPE: PRT
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RESULT 2
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| Sequence 2, Application US/10660763
| Publication No. US20040063130A1
| GENERAL IMFORMATION:
| APPLICANT: GAN, Weiniu et al.
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: THEREOF FILE REFERENCE: CLO01183DIVI CURRENT APPLICATION UNMBER: US/10/660,763
| CURRENT APPLICATION UNMBER: US/10/660,763
| CURRENT APPLICATION UNMBER: US/10/660,763
| CURRENT APPLICATION NUMBER: US/10/660,763
| CURRENT FILING DATE: 2003-09-12
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
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| TYPE: PRT
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                                                                                                       Conservative
                                                                                                   100.0%; Score 3879; DB 15; 100.0%; Pred. No. 2.8e-223; varive 0; Mismatches 0;
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                                                                                                   RESULT 3
US-10-003-295-4
; Sequence 4, Application US/10003295
; Publication No. US20020168741A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE OF INVENTION UNMBER: US/10/003,295
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTMARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; SEQ ID NO 4
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-295-4
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                                                                 Similarity
MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKMMAQRVKSDREYAGLLHHMSLQDSGGQS
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                                                    98.8%;
ilarity 91.5%;
Conservative
                                                    Score 3834; I
Pred. No. 1.5e
0; Mismatches
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                                                 DB 13;
1.5e-220;
hes 0;
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660

600 600

720 720 660 540 540 480 480 420 420

Length Indels

1

70;

Gaps

60

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APPLICANT: GAM, Weiniu et al.
APPLICANT: GAM, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PR
TITLE OF INVENTION: ACID MOLECULES ENCODING
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1183DIVII
CURRENT APPLICATION NUMBER: US/10/660,763
CURRENT FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 822
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                             RESULT 4
US-10-660-763-4
                                                                                                                                                                                                                    Sequence 4, Application US/10660763 Publication No. US20040063130A1 GENERAL INFORMATION:
                      -10-660-763-4
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Sequence 64, Application US/09886319A

Publication No. US20020086019A1

APPLICANT: Wolf, Eckard

APPLICANT: Werner, Sabine

APPLICANT: Halle, Jorn-Peter

APPLICANT: Regenbogen, Johannes

APPLICANT: Regenbogen, Johannes

APPLICANT: Roppelt, Andreas

TITLE OF INVENTION: Use of Polypeptides or Nucleic Aci
TITLE OF INVENTION: the Diagnosis or Treatment of Ski
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Pred. No. 1.
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Skin Disorders
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CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
ENOTH: 822
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Best Local Similarity
Matches 376; Conserv
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ORGANISM: Homo sapiens
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                                                                            ALEELKOSVOOLRCTEAKFSAOKELLEOKVOENDGKEPPPVVNYEEDARSVTSMERKE--
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                                                                                                                                         ETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGA 583
                                                                                                                                                                                      QVITKKSGVVLLNPIPKDKKWILSHEDVILGELLGKGNFGEVYKGTLK-DKTSVAVKTCK
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SSS-GLKQIPIKWTAPEALNYGRYSSESDVWSFGILLWETFSLGVCPYPGWTNQQAREQV
                                                                                                                        EDLPQELKIKFLQEAKILKQYDHPNIVKLIGVCTQRQPVYIIMELVSGGDFLTFLRRKKD
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APPLICANT: Regembogen, Johannes
APPLICANT: Goppelt, Andreas
ITITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
ITITLE OF INVENTION: Use of Polypeptides or Treatment of Skin Disorders and Wound
ITITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
ITITLE OF INVENTION: Healing and for the Identification of Pharmacologically
ITITLE OF INVENTION: Active Substances
FILE REFERENCE: 50128/014003
CURRENT APPLICATION NUMBER: US/10/376,564
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 09/886,319
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: US 100 30 149.5-41
PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
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Publication No. US20030180302A1
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APPLICANT: Werne
APPLICANT: Halle
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TYPE: PRT
ORGANISM: Homo
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Local Similarity 45.5%; Pred. No. 2.6e-102;
hes 376; Conservative 150; Mismatches 217;
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                                                                                         GRTPTLEILKSHISGIFR-PK----
                                                                                                                                        ALEELKQSVQQLRCTEAKFSAQKELLEQKVQENDGKEPPPVVNYBEDARSVTSMERKE--
                                            -RLSKFESIRHSIAGIIRSPKSAVGSSALSDMISISEKPLAEQDWYHGAIPRIEAQELLK
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Halle, Jorn-Peter
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APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 823
TYPE: DET
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US-09-886-319A-63
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         -09-886-319A-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
179
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HMLHNQYVLALKGAQLHQSQYYDTTLPLLLDSVQKMQEEMIKALKGIFDDYSQITSLVTE 238
                                                                                                    QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEA-SKDKDRDKAKDKYVRSLWKL
                                                                                                                                                                 VOVNYVSNVSKSWLLMIQQTEQLSRIMKTHAEDLNSGPLHRLTMMIKDKQQVKKSYVGIH 118
                                                                                                                                                                                                         RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSS-GLKQIPIKWTAPEALNYGRYSSESDVWSFGILLWETFSLGVCPYPGMTNQQAREQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVITKKSGVVLLNPIPKDKKWILSHEDVILGELLGKGNPGEVYKGTLK-DKTSVAVKTCK 594
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                                     FAHHNRYVIGVRAAQIHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQD 239
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                                                                              QQI EAEMI KVTKTELEKLKSSYRQLI KEMNSAKEKYKEALAKGKETEKAKERYDKATMKL
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                                                                                                                                                                                                                                                                                                                                   47.2%; Score 1829.5; DB 9; Length 823; 45.6%; Pred. No. 6.5e-101; ative 146; Mismatches 219; Indels 85;
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                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
ITILE OF INVENTION: Use of Polypeptides or Nucleic Acids for
ITILE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
ITILE OF INVENTION: Healing and for the Identification of Pharmacologically
ITILE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014003
CURRENT APPLICATION NUMBER: US/10/376,564
CURRENT APPLICATION NUMBER: US 09/886,319
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: DS 100 30 149.5-41
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
PRIOR FILING DATE: 2000-08-20
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
LENGTH: 823
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-376-564-63
Sequence 63, Application US/10376564
Publication No. US20030180302A1
GENERAL IMPORMATION:
APPLICANT: Wolf, Eckhard
APPLICANT: Werner, Sabine
; TYPE: PRT; ORGANISM: Mus musculus US-10-376-564-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FSNLYRLEGEGFPSIPLLIDHLLST 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RLSKFESIRHSIAGIIKSPKSVLGSSTQVCDVISVGERPLAEHDWYHGAIPRIEAQELL 475
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US-10-664-421-69
; Sequence 69, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREWER, RYAN
; APPLICANT: HERAHIM, PRABHA
; APPLICANT: KUMAR, ABHIMAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MIBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIL
; FILE REFERENCE: 039963/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
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PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 69
LENGTH: 292
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; ORGANISM: Homo
US-10-664-421-69
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US-10-763-418-38
                                                                                                       Query Match
Best Local S
Matches 274
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                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 275
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Best Local Similarity 99.7%;
Matches 291; Conservative
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APPLICANT: SCHLESSINGER, JOSEPH
APPLICANT: SCHLESSINGER, JOSEPH
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: US/10/763,418
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/664,526
PRIOR APPLICATION NUMBER: US/09/664,526
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR PILING DATE: 1998-11-09
PRIOR PILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1996-08-21
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ORGANISM: Homo
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                                               AVPKOKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLFPDLKAKFLQE
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nilarity 99.6%;
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Pred. No. 2e-83;
0; Mismatches 1;
                                                                                                         <u>,,</u>
                                                                                                         Score 1444; DB 16;
Pred. No. 1.9e-78;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: US/09/165,062
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 08/460,626
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 08/357,642
PRIOR FILING DATE: 1994-12-15
PRIOR FILING DATE: 1994-12-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 30
LENGTH: 251
                                                                         RESULT 12
US-08-987-689A-30
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US-10-464-805-30
                Sequence 30, Application US/08987689A Publication No. US20020048782A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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CURRENT APPLICATION NUMBER: US/10/464,805
CURRENT FILING DATE: 2003-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SCHLESSINGER, JOSEPH
TITLE OF INVENTION: PYK2 RELATED PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LEV, SIMA APPLICANT: SCHLESSINGER,
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TYPE: PRT
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Local Similarity 67.1%;
hes 169; Conservative 3
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                                                                                                                                                           NRPKFSDLHKEL 251
                                                                                                                                                                                                QRPSFSTIYQEL 744
                                                                                                                                                                                                                                                            VWSFGILLWETFSLGASFYPNLSNQQTREFVEKGGRLFCFELCFDAVFRLMEQCWAYEFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDA 597
                                                                                                                                                                                                                                         VWSFGILLWETFSLGVCPYPGMTNQQAREQVERGYRMSAPQNCPEEIFTIMMKCWDYKPE
                                                                                                                                                                                                                                                                                                                                                                                               IGVCTQRQPVYIIMELVPGGDFLSFLRKRKDELKLKQLVRFSLDVAAGMLYLEGKNCIHR
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Pred. No. 1.1e-46;
6; Mismatches 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 251;
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; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
US-08-987-689A-30
RESULT 13
US-10-292-524-30
; Sequence 30, Application US/10292524
; Publication No. US20030119067A1
; GENERAL INFORMATION:
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Best Local Similarity
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APPLICATION NUMBER: 60/032,824
FILING DATE: December 11, 196
APPLICATION NUMBER: 08/460,626
FILING DATE: June 2, 1995
APPLICATION NUMBER: 08/357,642
FILING DATE: December 15, 1994
ATTORNERY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90071
COMPUTER READBLE FORM:
COMPUTER: 3.5" Diskette, 1.44 Mb storage
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
OPERATING SYSTEM: IBM P.C. DOS 5.0
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LENGTH: 251 amino acid
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REFERENCE/DOCKET NUMBER: 23/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: December
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TITLE OF INVENTION: PYK2 RELATED PRODUCTS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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STATE: California
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                                                                                                                                                                              QRPSFSTIYQEL 744
                                                                                                                                                                                                                                                        VWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPG 732
                                                                                                                                                                                                                                                                                                                     DLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPBALNYGRYSSESD 672
                                                                                                                                                                                                                                                                                                                                                                          IGVCTOROPVYIIMELVPGGDFLSFLRKRKDELKLKQLVRFSLDVAAGMLYLEGKNGIHR
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                                                                                                                                         NRPKFSDLHKEL
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                                                                                                                                                                                                                   VWSFGILLWEIFSLGVCPYPGMINQQAREQVERGYRMSAPQNCPEEIFIIMMKCWDYKPE
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633 West Fifth
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.2%; Score 899; DB 8; 66.7%; Pred. No. 5.8e-46;
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APPLICANT: Sima Lev

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Best Local Similarity Matches 168; Conserv
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: December 15, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: PYK2 RELATED PRODUCTS AND METHODS
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240 NŘPKŘSDLHKĚĽ 251
                                                                                                                                                                                                                                                                                                                           553 IGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHR 612
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                                                                                                                                                                                                                          DLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYSSESD
                                                                                                                                                                                   DLAARNCLVGENNTLKISDFGMSRQEDGGVYSSS-GLKQIPIKWTAPEALNYGRYSSESD
                                         QRPSFSTIYQEL 744
                                                                                                                 VWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPG 732
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FILING DATE: 13-No. US20030119067A1-2002
CLASSIFICATION: <UNKNOWN>
                                                                                            VWSFGILLWETFSLGVCPYPGMTNQQAREQVERGYRMSAPQNCPEEIFTIMMKCWDYKPE 239
                                                                                                                                                                                                                                                                               IGVCTQRQPVYIIMELVPGGDFLSFLRKRKDELKLKQLVRFSLDVAAGMLYLEGKNGIHR
                                                                                                                                                                                                                                                                                                                                                                      LGELLGKGNFGEVYKGTLK-DKTPVAVKTCKEDLPQELKIKFLQEAKILKQYDHPNIVKL
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STATE: California
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STREET: 633 West Fifth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.2%; Score 899; DB 14; 66.7%; Pred. No. 5.8e-46; htive 36; Mismatches 46;
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-187-46
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CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 17.3%; Score 669.5; DB 10; Best Local Similarity 49.4%; Pred. No. 3e-32; Matches 128; Conservative 50; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Burgess, Catherine APPLICANT: Gusev, Vladimir Y
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SOFTWARE: PatentIn Ve
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239
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                                        726
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                                                                                                                             RYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQ 725
                                                                                                                                                                                                              KCCIHRDIAARNCIVTEKNVIKISDFGMSRE-EADGVYAASGGIRQVPVKWTAPEAINYG 665
                                                                                                                                                                                                                                                             NIVKLLGVCTEEEPLMIVMEYMEGGDLLDYLRKNRPNELSLSDLLSFALQIARGMEYLES
CWNEDPEDRPTFSELVERL
                                        CWAYEPGQRPSFSTIYQEL 744
                                                                                                                                                                        KNFVHRDLAARNCLVGENKTVKIADFGLARDLYDDDYYRVKGG--KLPVRWMAPESLKYG
                                                                                                                                                                                                                                                                                                                                              LTLGKKLGEGAFGEVYKGTLKGKGGKKVEVAVKMLKEDASESQIEEFLREAKIMRKLKHP
                                                                                   KFTSKSDVWSFGVLLWEIFTLGESPYPGMSNQEVLEYLKKGYRLPQPPNCPDEIYDLMKQ
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Shimkets, Richard A
Spaderna, Steven K
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Padigaru, Muralidhar
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PRIOR APPLICATION NUMBER: 60/263,135
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,688
PRIOR FILING DATE: 2001-01-24
PRIOR REPLICATION NUMBER: 60/263,694
PRIOR REFLING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Pacentin Ver. 2.1
SEG ID NO 42
LENGTH: 257
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/863,776
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Majumder, Kumud
APPLICANT: Tchernev, Velizar T
APPLICANT: Mishra, Vishnu
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PRIOR APPLICATION NUMBER: 09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/206,679
PRIOR FILING DATE: 2000-05-24
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PRIOR APPLICATION NUMBER: 60/221,927
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APPLICATION NUMBER: 60/209,451
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APPLICATION NUMBER: 60/206,829
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                                  548 NIVRLIGVCTQKQPIVIVMELVQGGDFLTFLRTEGAR-LRVKTLLQMVGDAAAGMEYLES 606
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Spaderna, Steven K
Shenoy, Suresh G
Rastelli, Luca
LTLGKKLGEGAFGEVYKGTLKGKGGKEVEVAVKTLKEDASEQQIEEFLREAKIMRKLDHP
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361 QEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLLQDDRHSTSSSEQEREGGR	301 LTVESVOHTLTSVTDELAVATEMVFRROEMVTQLQOELRNEEENTHPRERVQLLGKRQVL 	241 VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE 	181 AHHNRYVLGVRAAQLHHQHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQ 	121 QOLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKL 	61 RAISPDSPISQSWABITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 	1 MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQ 	100.0%; Score 3879; DB 3; Length 752; set Local Similarity 100.0%; Pred. No. 1.1e-261; atches 752; Conservative 0; Mismatches 0; Indels 0; Gaps	180-2 2, Application US/09817180 10. 6340584 INFORMATION: INT: GAN, Weiniu et al. NUT: GAN, Weiniu et al. PINVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC PINVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, PINVENTION: THEREOF PERENCE: CL001183 2 APPLICATION NUMBER: US/09/817,180 2 FILING DATE: 2001-03-27 00 SEQ ID NOS: 4 18: PSEQ ID NOS: 4 18: PSEQ ID NOS: 4 18: PSEC SEQ ID NOS: 4 18: PSEC SEC SEQ ID NOS: 4 18: PSEC SEC SEQ ID NOS: 4 18: PSEC SEC SEQ ID NOS: 4 18: PS	ALIGNMENTS	8 597 15.4 527 5 PCT-US95-05008-10 Sequence 10, 9 596.5 15.4 386 4 US-09-741-154-4 Sequence 2, 15.96.5 15.4 415 4 US-09-741-154-2 Sequence 2, 15.93.5 15.3 661 4 US-09-949-016-1329 Sequence 2, 15.93.5 15.3 661 4 US-09-949-016-6325 Sequence 63.5 15.2 594 4 US-09-949-016-7838 Sequence 5, 15.2 594 4 US-09-949-016-7838 Sequence 7, 15.2 594 4 US-09-949-016-7838 Sequence 7, 15.2 594 5 US-08-426-599A-4 Sequence 4, 15.2 675 3 US-08-426-599A-4 Sequence 4, 15.2 675 3 US-08-426-599A-9 Sequence 4, 15.2 620 4 US-08-232-545-4 Sequence 4, 15.2 620 3 US-08-426-599A-9 Sequence 9, 15.2 620 3 US-08-426-599A-9 Sequence 9, 15.2 620 4 US-08-232-545-9 Sequence 9, 15.2 620 4 US-08-316-33 Sequence 9, 15.2 620 4 US-08-316-33 Sequence 3, 15.1 1053 3 US-08-63-118-3 Sequence 3, 15.1 1053 3 US-08-63-118-3 Sequence 3, 15.1 620 4 US-09-949-016-6626 Sequence 4, 15.1 10.5 3 US-08-63-118-3 Sequence 4, 15.1 10.5 15.0 680 3 US-08-160-861-4 Sequence 4, 15.1 10.5 15.0 680 3 US-08-160-861-4 Sequence 4, 15.1 15.0 680 3 US-09-100-089-4 Sequence 4, 15.1 15.1 15.1 15.1 15.1 15.1 15.1 15.
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GENERAL INFORMATION:

APPLICANT: GAN, Weiniu et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLIOO1183DIV

CURRENT APPLICATION NUMBER: US/10/003,295

CURRENT FILING DATE: 2001-12-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASUSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 752

TYPE: PRT

ORGANISM: Homo sapiens

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                                                VVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLNE
                                                                                                           AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE
                                                                                                                            AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE
                                                                                                                                                                                        QQLQQELTXTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF
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Best Local S
Matches 752
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TITLE OF INVENTION: ASCLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ASCLD MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183
CURRENT FILING DATE: US/09/817,180
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 8822
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09817180 Patent No. 6340584 GENERAL INFORMATION:
                   241
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QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
                                                                                                                                                                        RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
                                                                                                                                                                                         RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
                                                                                                                                                                                                                                     MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
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                                              AHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHBEMACILKBILQEYLEISSLVQDB
                                                                AHNRYVLGVRAAQLHHQHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQDE
                                                                                                           QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF
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                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                           98.8%;
91.5%;
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Pred. No. 1.6e-258;
0; Mismatches 0;
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APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUI
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINA
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183DIV
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 822
TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. 6686187
GENERAL INFORMATION:
                                                                                                                                                                     Matches
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QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
                                                               RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
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                                                                                                        MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
                                                                                                                                                                     Conservative
                                                                                                                                                                                  98.8%;
91.5%;
                                                                                                                                                                  Score 3834; DB 4;
Pred. No. 1.6e-258;
0; Mismatches 0;
                                                                                                                                                                                                  DB 4; Length
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                                                                                                      Sequence 866, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and
FILE REFERENCE: 15966-542
CURRENT FILING DATE: 2000-03-29
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SUFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 866
LENGTH: 822
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US-09-538-092-866
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FRATURE:

FRATURE:

LOCATION: (0)...(0)

OTHER INFORMATION: Polypeptide Accession Number P07332
                                                                          LENGTH: 822
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 64, Application U
Patent No. 6586185
GENERAL INFORMATION:
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabin
APPLICANT: Halle, Jorn-P
APPLICANT: Regenbogen, J
APPLICANT: Goppelt, Andr
TITLE OF INVENTION: Use o
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US-09-886-319A-64
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T: Werner, Sabine
T: Halle, Jorn-Peter
T: Regenbogen, Johannes
T: Goppelt, Andreas
'INVENTION: Use of Polypeptides
                                                                                                                                   CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
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Conservative
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Pred. No. 4.2e-258;
   or Nucleic
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EDLPQELKIKFLQEAKILKQYDHPNIVKLIGVCTQRQPVYIIMELVSGGDFLTFLRRKKD

654

594 523 535

KQGDFLVRESHGKPGEYVLSVYSDGQRRHFIIQYVDNMYRFEGTGFSNIPQLIDHHYTTK

-- FSNLYRLEGEGFPSIPLLIDHLLSTQ

464

475 438 416

VIQEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLLQDDRHSTSSSEQEREG

418

358

GRTPTLEILKSHISGIFR-PK-------ALEELKOSVOOLRCTEAKFSAOKELLEOKVOENDGKEPPPVVNYEEDARSVTSMERKE--

-RLSKFESIRHSIAGIIRSPKSAVGSSALSDMISISEKPLAEQDWYHGAIPRIEAQELLK

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US-09-886-319A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound TITLE OF INVENTION: Healing and for the Identification of Pharmacologically TITLE OF INVENTION: Active Substances FILE REFERENCE: 50125/014002

CURRENT APPLICATION NUMBER: US/09/886,319A

CURRENT FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: US 60/222,081

PRIOR APPLICATION NUMBER: US 60/222,081

PRIOR APPLICATION NUMBER: DE 10030149.5

PRIOR APPLICATION NUMBER: DE 10030149.5

PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 822
TYPE: PRT
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 47.8%; Score 1853; DB 4; Length Similarity 45.5%; Pred. No. 1e-120;
                                                                                                                                                                                                                                                                                                  ELTVESVQHTLTSVTDELAVATEMVFRRQEMVTQLQQELRNEEENTHPR-ERVQLLGKRQ
                                                                                                BVVAIHREMAAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLBEGEPLEPGELQLN
                                                                                                                                                 QQIBABMIKVTKTELEKLKCSYRQLIKEMNSAKEKYKBALAKGKETEKAKERYDKATMKL
                                                                                                                                                                                                                                                    QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEA-SKDKDRDKAKDKYVRSLWKL
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                                                                                                                                                                                                                                                                                                                                                                              MGFGSDL--KNSHEAVLKLQDWELRLLETVKKFMALRIKSDKEYASTLQNLCNQVDKEST
                                                                                                                                                                                                                                                                                                                                                                                                   MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
                                                                             EIVNVHKEIOMSVEQIDPSTEYNNPIDVHRTTAAKEQEIEPDTSLLEENENLOANEIMWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     150; Mismatches 217;
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EKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKR

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APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
ITITLE OF INVENTION: Protein-Protein Complexes and
FILE REFERENCE: 1596-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPALSeqFormatter Version 0.9
158Q ID NO 941
LEWICTH. 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P16591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 822
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
 476
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KQGDFLVRESHGKPGEYVLSVYSDGQRRHFIIQYVDNMYRFEGTGFSNIPQLIDHHYTTK
                                                                                                                                         ALEELKOSVOOLRCTEAKFSAOKELLEOKVOENDGKEPPPVVNYEEDARSVTSMERKE--
                                                                                                                                                            VLQEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLLQDDRHSTSSSEQEREG
                                                                                                                                                                                                                                              ELTVESVOHTLISVIDELAVATEMVFRRQEMVIQLQQELRNEEENTHPR-ERVQLLGKRQ 358
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                                                                                                    GRIPTLEILKSHISGIFR-PK------
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                                                                    -RLSKFESIRHSIAGIIRSPKSAVGSSALSDMISISEKPLAEQDWYHGAIPRIEAQELLK 475
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45.5%; Pred. No. 1e-120;
vative 150; Mismatches 217; Indels 84;
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                                 ----FSNLYRLEGEGFPSIPLLIDHLLSTQ 464
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APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
TITLE OF INVENTION: Hallengnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILTE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER: DE 10030149.5
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US-09-886-319A-63
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Best Local S
Matches 377
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 63
LENGTH: 823
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Patent No. 6
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APPLICANT: Werne
APPLICANT: Halle
                                                                                                                                                                                                                                                                                                                                                                          / Match 47.2%; Score 1829.5; DB 4; Length Local Similarity 45.6%; Pred. No. 4.4e-119; nes 377; Conservative 146; Mismatches 219; Indels
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                                                                                                                                                                       QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEA-SKDKDRDKAKDKYVRSLWKL 179
                                                                                                                                                                                                                    VQVNYVSNVSKSWLLMIQQTEQLSRIMKTHAEDLNSGPLHRLTMMIKDXQQVKKSYVGIH 118
                                                                                                                                                                                                                                          RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW 120
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EIVNVHKEIOMSVEOIDPSTEYNNFIDVHRTTAAKEQEIEFDTSLLEENENLOANEIMWN
                                 EVVAIHREMAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLN 299
                                                                        HMLHNQYVLALKGAQLHQSQYYDTTLPLLLDSVQKMQEEMIKALKGIFDDYSQITSLVTE
                                                                                                                                                 QQIEAEMIKVTKTELEKLKSSYRQLIKEMNSAKEKYKEALAKGKETEKAKERYDKATMKL
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RESULT 9
US-08-701-191A-38
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Patent No. 5942428
                                                                                                                                                                                       ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mooba Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 41
                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                     FILING DATE: August 21, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEG 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQQGDFLVRESHGKPGEYVLSVYSDGQRRHFIIQFVDNLYRFEGTGFSNIPQLIDHHFNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERGYRMSAPONCPEEVFTIMMKCWDYKPENRPKFNDLHKELTVIKK 820
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APPLICANT: MCHAMMADI, MCOSA
APPLICANT: SCHLESSINGER, JOSEPH
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOW
TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOW
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: US/09/664,526
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SOPTWARE: PATENTIN VET: 2.1
SEQ ID NO 38
LENGTH: 275
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TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-701-191A-38
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
                                                                                                                             Query Match
Best Local Simi
Matches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38, Applical Patent No. 6682921 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.2%;
Best Local Similarity 99.6%;
Matches 274; Conservative
                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo
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Similarity 99.6%;
ARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDA
                                                                           AVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQE
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                                                       AVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09664526
                                                                                                                                 Conservative
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Pred. No. 7.4e-93;
0; Mismatches 1;
                                                                                                                             Score 1444; DB 4; Pred. No. 7.4e-93; 0; Mismatches 1;
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                                                                                                                                                                 Length 275;
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US-07-857-224B-62
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                                                                   Query Match 35.2%;
Best Local Similarity 99.6%;
Matches 262; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (International TELEX: none INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 262
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APPLICANT: Benner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Switzerland
ZIP: (note: this is an international post code)
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                ORGANISM: human FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 28
TELEFAX: (International) 41 1 262 2437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                AUTHORS: Hunter, AUTHORS: The protein kinase
                                                                                                                                                                                                                                                            AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
                                                                                                                                                              PAGES: 42-52
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
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                                489
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                 EDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHPN 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVFRLMEQCWAYEPGORPSFSTIYQELQSIRKRHR 752
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                                                                   Score 1364.5; DB 2;
Pred. No. 2.4e-87;
0; Mismatches 0;
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                                                                     Indels
                                                                                                      Length
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SEQUENCE CHARACTERISTICS:
LENGTH: 262
TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 63, Application US/07857224B Patent No. 5958784
Query Match
Best Local Similarity 97.
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                         AUTHORS: Qu.....,
AUTHORS: Hunter, T.
AUTHORS: Hunter, T.
TITLB: The protein kinase fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple MacIntosh 7.0 OPERATING SYSTEM: MacIntosh 7.0 SOFTWARE Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: (note: this is an international post code) CH-8092 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Benner, Steven A. TITLE OF INVENTION: Predicti
                                                                                                                                                                                                                                     FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                        DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                       AUTHORS:
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Hadlaubstrasse 151
                                                                                                                                                                   Hanks, S. K.
Quinn, A. M.
Hunter, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Switzerland
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               34.8%; Score 1350.5; DB 2; 97.7%; Pred. No. 2.2e-86;
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   4.
                                                                                                                                                     family
Mismatches
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   Indels
                                 Length 262;
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   Gaps
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US-07-857-224B-64
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US-07-857-224B-64
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                                                                                                                                                                                                                                                                                                                                  TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: TONE
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (International) 41 1 632 2830
TOTREPHONE: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Benner, Steven A. TITLE OF INVENTION: Predicti
                                                                                                                                                                          FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (International) 41 1
                                                 JOURNAL: Sc.
VOLUME: 241
                                                                                  AUTHORS: Hanke, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
                PAGES: 42-1
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 03
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Switzerland
                                                                                                                                                           AUTHORS:
                                                                                                                                                                                                           ORGANISM: chicken
                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                    LENGTH:
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Query Match

28.8%;

Score 1116.5;

DB 2;

Length 262;

RESULT 15

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US-10-003-690-8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 79.8 Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/003,690
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/248,893
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROTY A.J. Curtis
TITLE OF INVENTION: 55053, A No. 6787345el Human Eukaryotic
TITLE OF INVENTION: and Uses Therefor
FILE REFERENCE: MNI-206
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                    Local
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 234
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                               GGRLPCPE-----LCPDAVFRLMEQCWAYEPGQRPSFSTIYQEL 744
                                                                  LLPIRWMAPESLKDGKFTSKSDVWSFGVLLWEIFTLGEQPYPGBIQQFMSNEBVLEYLKK
                                                                                            QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPN-----LSNQQTREFVEK 705
                                                                                                                                    EYLESKNFVHRDLAARNCLVGENKVVKISDFGLSRDLYDDDKKGESKDYYRKKGGKGGKT 173
                                                                                                                                                     BYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSRE-----EADGVY---AASGGLR 650
                                                                                                                                                                                                      İVKLLGVCTEEGRRFMEVEPLMİVMEYMEGGDLLDYLRKNRPKLSLSDLLSFALQIAKGM 113
                                                                                                                                                                                                                     IVRLIGVCTQK-----QPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAGM 601
                                                                                                                                                                                                                                                                    LTLGKKLGEGAFGEVYKGTLKIE---VAVK----TLKEDAKEEFLREAKIMKKLGGKHPN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEPGORPSFSTIYOELOSIRKRH 751
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 GYRLPKPENDLPISSVTCPDELYDLMLQCWAEDPEDRPTFSELVERL
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                                                                                                                                                                                                                                                                                                                                                    16.6%; Score 642; DB 4; 46.3%; Pred. No. 4.7e-37;
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29; Mismatches 23;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOPTWARE: FABLUSEQ for Windows Version 4.0
SEQ ID NO 6798
LENGTH: 1148
TYPE: PRT
ORGANISM: Human
US-09-949-016-6798
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOO1307
Search completed: March 18, 2005, 16:01:08 Job time: 57 secs
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2: pir2:*
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14.9	14.9	14.9	14.9	14.9	15.0	15.0	15.0	15.0	15.0	15.1	15.2	15.2	15.2	15.3	15.4
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A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; F;2-822/Product: protein-tyrosine kinase fes/fps #status predicted <MAT> F;260-545/Domain: SH2 homology <SH2> F;460-545/Domain: SH2 homology <SH2> F;559-821/Domain: protein kinase homology <KIN> F;559-821/Domain: protein kinase homology <KIN> F;557-575/Region: protein kinase homology chinating motif F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted F;590/Active site: Lys #status predicted
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A; Molecule type: mRNA
A; Residues: 1-718, 'S', 720-822 <ALC>
A; Cross-references: GB: X52192; NID: g29890; PIDN: CAA36438.1; PID: g29891
A; Cross-references: GB: X52192; NID: g29890; PIDN: CAA36438.1; PID: g29891
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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24673; A60188
C;Accession: A24673; A60188
R;Rosbroek, A.J.M.; Schalken, J.A.; Verbeek, J.S.; Van den Ouweland, A.M.W.; Onnekink,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P07332; GB:X06292; GB:M14209; GB:M14589; NID:g31348; PIDN:CALR; Alcalay, M.; Antolini, F.; Van de Ven, W.J.; Lanfrancone, L.; Grignani, F.; Pelicci, P. Oncogene 5, 267-275, 1990
A;Title: Characterization of human and mouse c-fee cDNA clones and identification of the A;Reference number: A60188; MUID:90191711; PMID:2179816
A;Accession: A60188
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A;Map position: 15q26.1-15q26.1
A;Introns: 71/3; 129/3; 162/1; 223/2; 269/2; 309/2; 350/2; 412/3; 440/3; 510/3; 51/3;
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QQLQQELTKTHSQDIEKLKSQYRALARDSAQAKRKYQEASKDKDRDKAKDKYVRSLWKLF 180
                                                                                                     RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
                                                                                                                                                                                       MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS
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                                                                 RAISPDSPISQSWAEITSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKTYSEQW
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Pred. No. 7.8e-141;
0; Mismatches 0;
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protein-tyrosine kinase (EC 2.7.1.112) fes/fps - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 30-Sep-1989 #sequence_revision 30-Jun-1992 #text_change 23-Feb-1997
C;Accession: A27824
R;Roebroek, A.J.M.; Schalken, J.A.; Omnekink, C.; Bloemers, H.P.J.; Van de Ven, W.J.:
J. Virol. 61, 2009-2016, 1987
J. Virol. 61, 2009-2016, 1987
A;Title: Structure of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps proto-oncogene: genesis of a retroviral on the complex of the feline c-fes/fps 
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93.3%;
85.8%;
Score 3620; DB 1;
Pred. No. 1.3e-132;
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                                                                                                                                                                     KAKFLQEAKILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRMKTL
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protein-tyrosine kinase-related protein K,Alternate names: c-fes protein C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision (C;Accession: 18347; JH0112 02-Jul-1996

#text_change

mouse

R;Wilks, A.F.; Kurban, R.R.
Oncogene 3, 289-294, 1988
A;Title: Isolation and structural analysis
A;Reference number: I48347; MUID:89083198;
A;Accession: I48347
A;Status: preliminary; translated from GB/E
A;Molecule type: mRNA GB/EMBL/DDBC of murine c-fes PMID:3060793

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A;Molecule type: mRNA
A;Residues: 678-745 <WIL>
A;Experimental source: haemopoietic cell, clone FD15
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
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F;458-543/Domain: SH2 homology <SH2>
F;557-819/Domain: protein kinase hom
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A;Cross-references: UniPROT:P16879; EMBL:X12616; NID:g50955; PIDN:CAA31138.1; R;Wilke, A, F.; Kurban, R.R.; Hovens, C.M.; Ralph, S.J.

Gene 85, 67-74, 1989
A;Title: The application of the polymerase chain reaction to cloning members chaired enumber: JH0112; MUID:90152381; PMID:2482828
A;Accession: JH0112
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                                                                                                                                                                                             SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL
                                                                                                                                                                                                                                             -----NLYRLEGEGFPSIPLLIDHLLSTQQPLTKK
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 CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
                          QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLTNQQTREFVEKGHRLP
                                       QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP
                                                                          LQMMGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGIYAACSGLR
                                                                                         LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR
                                                                                                                           KAKFLQEARILKQYNHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL
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A;Gross-references: UNIPROT:Q90778; EMBL:X02266; NID:g63203; PIDN:CAA26155.1; PID:g8710 C;Genetics:
A;Genetics:
A;Gene: c-fps
A;Introns: 75/3; 13/3; 166/1; 227/2; 273/2; 313/2; 354/2; 416/3; 442/3; 512/3; 553/3; C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology C;Keywords: ATP:C;Keywords: ATP:Domain: SH2 homology <SH2>
F;462-547/Domain: SH2 homology <SH2>
F;561-823/Domain: protein kinase homology <KIN>
F;569-577/Region: protein kinase ATP-binding motif
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J. Mol. Biol. 181, 175-186, 1985
A;Title: Nucleotide sequence and topography of chicl
A;Reference number: I50618; MUID:85160839; PMID:387;
A;Accession: I50618
A;Status: preliminary; translated from GB/EMBL/DDBJ
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c;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: I50618
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A; Residues: 1-824 < HUA>
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                                                                                                             SGDFLVRESQGKQEYVLSVLWDGQPRHFIIQAADNLYRLEGDGFPTIPLLIDHLLQSQQP
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C;Species: Pujinami sarcoma virus
C;Species: Pujinami sarcoma virus
C;Species: Pujinami sarcoma virus
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26898
R;Ghen, L.H.; Hatada, E.; Wheatley, W.; Lee, W.H.
Virology 155, 106-119, 1986
A;Title: Single amino acid substitution, from Glu-1025 to Asp, of the fps oncogenic prot
A;Reference number: A26898; MUID:87044080; PMID:2877522
A;Accession: A26898
A;Accession: A26898
A;Accession: A26898
A;Accession: A26898
A;Accession: This protein is synthesized as a gag-fps polyprotein.
C;Comment: This protein is synthesized as a gag-fps polyprotein.
C;Coment: This protein is synthesized as a gag-fps polyprotein.
C;Genetics:
A;Gene: fps
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
F;610-872/Domain: protein kinase homology <KIN>
F;618-626/Region: protein kinase ATP-binding motif
F;641/Active site: Lys #status predicted
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3.5e-92;
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C;Genetics:
A;Genetics:
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A;Reference number: A00636; MUID:83050964; PMID:6291784
A;Accession: A00636
A;Molecule type: genomic RNA
A;Residues: 1-873 <SHI>
A;Cross-references: UNIPROT:P00530
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protein-tyrosine kinase (EC 2.7.1.112) fes - feline sarcoma virus
C;Species; feline sarcoma virus
A;Note: host Felis sp. (cat)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change |
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change |
C;Caccession: A00651
R;Hampe, A.; Laprevotte, I.; Galibert, F.; Fedele, L.A.; Sherr, (cell 30, 775-785, 1982
A;Title: Nucleotide sequences of feline retroviral oncogenes (v-1)
A;Reference number: A00651; MUID:83050983; PMID:6183005
A;Reference number: A00651; MUID:83050983; PMID:6183005
A;Residues: 1-609 <HAM>
A;Residues: 1-609 <HAM>
A;Cosse-references: UNIPROT:P00542
C;Comment: This protein is synthesized as a gag-fes polyprotein.
                                                                                                     A;Gene: fes
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase;
F;247-332/Domain: SH2 homology <SH2>
F;247-332/Domain: protein kinase homology <KIN>
F;346-608/Domain: protein kinase homology <KIN>
F;354-362/Region: protein kinase ATP-binding motif
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MGFSSELCSPQGHGAEQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDGGG--
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                                                     Conservative
                                                                  63.9%; Score 2479; DB 1; 61.7%; Pred. No. 7.8e-89;
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                  CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
                                                                                              QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP
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CPELCPDAVFRLMEQCWAYEPGQRPSFSAIYQELQSIRKRHR
                                                                            QVPVKWTAPEALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLP
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protein-tyrosine kinase (EC 2.7.1.112)
C;Species: feline sarcoma virus
A;Note: host Felis sp. (cat)
C;Date: 27.Nov-1985 #sequence_revision
C;Accession: A00652
R;Hampe, A.; Laprevotte, I.; Galibert, |
Cell 30, 775-785, 1982 A; Molecule type: DNA A; Residues: 1-477 <HAM> A; Cross-references: UNIPROT: P00543 C; Comment: This protein is synthesized C; Genetics: A; Gene: fee C; Superfamily: protein-tyrosine kinase Cell 30, 775-785, 1982
A;Title: Nucleotide sequences of feline retroviral oncogenes (v-fes)
A;Reference number: A00651; MUID:83050963; PMID:6183005 A; Accession: A00652 A.; Laprevotte, I.; Galibert, F.; 775-785, 1982 fes 98 27-Nov-1985 #text_change מפ • Fedele, L.A.; Sherr, C. gag-fes feline sarcoma virus (strain Snyder-Theilen) polyprotein 09-Jul-2004 provide evidence

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protein-tyrosine kinase (EC 2.7.1.112) fer - human (;Species: Homo sapiens (man) (;Chate: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-C;Accession: A31943; IS7573 R;Hao, Q.L.; Heisterkamp, N.; Groffen, J. Mol. Cell. Biol. 9, 1587-1593, 1989 A;Title: Isolation and sequence analysis of a novel human tyrosine A;Reference number: A31943; MUID:89261786; PMID:2725517 A;Accession: A31943.
                   F;561-821/Domain: protein kinase homology <KIN>
F;569-577/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (ir
F;591/Active site: Lys #status predicted
                                                                                                  A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; F;2-822/Product: protein-tyrosine kinase fer #status predicted <MAT> F;460-546/Domain: SH2 homology <SH2>
                                                                                                                                                                                                          A;Cross-references:
A;Map position: 5q12
C;Function:
                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-822 <HAO>
A; Cross-references: UNI
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5q12-5q14
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Pred. No. 9.7e-70;
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A;Title: Nucleotide sequence of v-fps in the PRCII strain A;Reference number: A00650; MUID:84138803; PMID:6321783 A;Accession: A00650
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Query

Match

47.8%;

Score 1853;

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Length

A; Molecule type:

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avian

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В
protein-tyrosine kinase (EC 2.7.1.112) C;Species: avian sarcoma virus PRCII A;Note: host Gallus gallus (chicken) C;Date: 27-Nov-1985 #sequence_revision C;Accession: A00650 R;Huang, C.C.; Hammond, C.; Bishop, J.W. virol. 50, 125-131, 1984
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protein-tyrosine kinase (EC 2.7.1.112), fps/fes homolog - fruit fly (Dr N;Alternate names: kinase-related transforming protein (fps) C;Species: Drosophila melanogaster C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-C;Accession: A39670; S1658 R;Katzen, A.L.; Montarras, D.; Jackson, J.; Paulson, R.F.; Kornberg, T. Mol. Cell. Biol. 11, 226-239, 1991 Mol. Cell. Biol. 11, 226-239, 1991 A;Title: A gene related to the proto-oncogene fps/fes is expressed at d A;Reference number: A39670; MUID:91094836; PMID:1898762 A;Accession: A39670 A;Molecule type: mRNA A;Residues: 1-803 <KA2> A;Cross-references: UNIPROT:P18106; EMBL:X52844; NID:g7971; PIDN:CAA370 C;Genetics: UNIPROT:P18106; EMBL:X52844; NID:g7971; PIDN:CAA370 C;Genetics:
A;Gene: dfps85D
A;Cross-references: FlyBase:FBgn0000723
A;Cross-references: FlyBase:FBgn0000723
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-or
F;438-525/Domain: SH2 homology <SH2>
F;438-525/Domain: SH2 homology <SH2>
F;539-799/Domain: protein kinase homology <KIN>
F;547-555/Region: protein kinase ATP-binding motif
F;570/Active site: Lys #status predicted
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A;Cross-references: UNIPROT: P00541
C;Comment: This protein is synthesized as a gag-
C;Genetics:
A;Gene: ips
C;Superfamily: protein-tyrosine kinase ips; prot
C;Keywords: ATP; autophosphorylation; oncogene;
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Pred. No. 2.6e-49;
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ene; phosphoprotein; phosphotransferase;
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IDTGYRMPTPKSTPEEMYRLMLQCWAADAESRPHFDEIYNVVDAL
                              VEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSI
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protein-tyrosine kinase (EC 2.7.1.112) flk - rat (fragme C;Species: Rattus norvegicus (Norway rat) C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text C;Accession: S04328 R;Letwin, K.; Yee, S.P.; Pawson, T. Oncogene 3, 621-627, 1998 A;Title: Novel protein-tyrosine kinase cDNAs related to A;Reference number: S04327; MUID:94167102; PMID:2485255 A;Accession: S04328
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A;Molecule type: mRNA
A;Residues: 1-323 <LET>
A;Cross-references: UNIPROT:P09760; EMBL:X13412; NID:g56169; PIDN:CAA31778.1;
C;Genetics:
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A;Title: A murine fer testis-specific transcript (ferT) encodes a truncated A;Reference number: I49663; MUID:90097822; PMID:2294399
A;Accession: I49663
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A;Molecule type: mRNA
A;Residues: 1-453 <RES>
A;Cross-references: UNIPROT:Q61561; GB:M32054; NID:g193276; PIDN:AAA37617.1; PID:g309235
C;Superfamily: protein kinase homology; SH2 homology
C;Superfamily: protein kinase homology; SH2 homology
C;Stypords: ATP
F;91-177/Domain: SH2 homology <SH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine kinase (ferT) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C;Accession: I49663
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C;Superfami
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Best Local S
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                                                                                                                                                                      348 RERVQLLGKRQVLQEALQGLQVALCSQAKLQAQQELL--QTKLEHLGPGEPPPVLLLQDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLYRLEGEGFPSIPLLIDHLLSTQQPLTKKSGVVLHRAVPKD-KWVLNHEDLVLGEQIGR
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    GFPSIPLLIDHLLSTQQPLTKKSGVVLHRAVPKD-KWVLNHEDLVLGEQIGRGNFGEVFS
                                          WYHGAI PRIEAQELLKQQGDFLVRESHGKPGEYVLSVYSDGQRRHFIIQFVDNLYRFEGT
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                                                                                                                                                                                                                                       28.3%; Score 1097; DB 2; 53.3%; Pred. No. 8.6e-36;
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66.2%; Pred. No. 4.96
tive 45; Mismatches
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lee 57;
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proto-fps protein - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_chan
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_chan
C;Accession: I50406
R;Pfaff, S.L.; Zhou, R.
Virology 146, 307-314, 1985
A;Title: Defining the borders of the chicken proto-fps gene,
A;Title: Defining the borders of the chicken proto-fps gene,
A;Reference number: I50405; MUID:86020620; PMID:2996222
A;Accession: I50406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
gag-abl-pol polyprotein - feline sarcoma virus (strain N;Contains: protein-tyrosine kinase (EC 2.7.1.112) C;Species: feline sarcoma virus C;Date: 31-Dec-1988 #sequence_revision 09-Sep-1994 #tex C;Accession: A26132
                                                                                            RESULT
A26132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: protein-tyrosine kinase fps; protein kina
C;Keywords: ATP
F;1-180/Domain: protein kinase homology (fragment) <KIN>
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C;Genetics:
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A; Residues: 1-181 < PFA>
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73.5%; Pred. No. 3.2e-22;
ative 26; Mismatches 22
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Sarc

09-Sep-1994 #text_change

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R;Bergold, P.J.; Blumenthal, J.A.; D'Andrea, E.; Snyder, H.W.; Lederman, L.; Silverstond J. Virol. 61, 1193-1202, 1987
A;Title: Nucleic acid sequence and oncogenic properties of the HZ2 feline sarcoma virus A;Reference number: A26132; MUID:87141338; PMID:3029415
A;Accession: A26132
A;Molecule type: DNA
A;Residues: 1-697 <BER>
A;Cross-references: GB:M15805; NID:g323883; PIDN:AAA43042.1; PID:g323884
C;Genetics:
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(;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
(;Superfamily: unassigned Ser/Thr or Tyr-specific protein; transforming protein; tyrosi
(;Keywords: ATP; oncogene; phosphotransferase; polyprotein; tyrosi
(;Keywords: ATP; oncogene; phosphotransferase; phosphotransferas
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ALIGNMENTS

09-APR-2002 ABB07354 standard; Human proto-oncogene tyrosine kinase ABB07354; (first entry) protein; 752 B

gene therapy; anti-kinase. Proto-oncogene tyrosine kinase; poTK; tumour; cytostatic; anti-leukemic; gene therapy; protein therapy; vaccine; enzymatic-inhibition; human;

Homo sapiens.

US6340584-B1.

22-JAN-2002

27-MAR-2001; 2001US-00817180.

27-MAR-2001; 2001US-00817180

(PEKE) PE CORP NY.

Ye J, Di Francesco < Beasley EM;

WPI; 2002-138497/18. N-PSDB; ABA94500, ABA94501.

Nucleic acids encoding a proto-oncogene tyrosine kinase, prevention, diagnosis and treatment of e.g. leukemia and useful for the lung tumors.

Claim 1; Fig 2A; 49pp; English.

The invention provides isolated nucleic acid sequences encoding a protooncogene tyrosine kinase (poTK). The poTK polynucleotides and protein may
be used in the prevention, diagnosis and treatment of diseases associated
with inappropriate poTK expression, such as lung and kidney tumours,
leukemia and stomach adenocarcinoma. poTK may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of poTK by expressing
inactive proteins or to supplement the patients own production of poTK.
The encoded poTK may be used as an antigen in the production of
antibodies against poTK and in assays to identify modulators of poTK
expression and activity. The anti-poTK antibodies and antagonists may be
used to down regulate expression and activity and as diagnostic agents

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Matches 752
 Human; kinase; proto-oncogene tyrosine kinase; antiarteriosclerotic;
                              Human kinase
                                                                                       ABB99046
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al Similarity 100.0%;
752; Conservative
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Pred. No. 6e-280;
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MGFSSELCSPQGHGVLQQMQEAELRLLEGMRKWMAQRVKSDREYAGLLHHMSLQDSGGQS

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Query Match Best Local Simi Matches 752;

Similarity

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Score 3879; Pred. No. 6e Mismatches

6e-280; BB <u>,,</u> 6

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Sequence 752 AA;

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The invention relates to a newly isolated peptide sequence of a human CC kinase that is related to the proto-oncogene tyrosine kinase subfamily. CC The activity of the kinase of the invention may be described as, CC cytostatic, antiarteriosclerotic, antiinflammatory and antipsoriatic. CP peptides of the invention are useful in assays to determine the CC biological activity of the protein, in drug screening assays, tissue CC typing and pharmacogenomic analysis. They are also useful in treating or CC diagnosing disorders characterised by an absence of, inappropriate, or CC unwanted expression of the protein, such as inflammation, cancer (e.g. CC leukaemia, lung tumours, kidney tumours or stomach adenocarcinoma), CC arteriosclerosis, and psoriasis Nucleic acid molecules of the invention CC are useful as probes, primers and chemical intermediates in biological CC assays. The peptide and nucleic acid sequences are useful as models for the development of human therapeutic targets, aid in the identification of the development of human therapeutic targets, aid in the identification CC therapeutic proteins and serve as targets for the development of human therapeutic protein activity in cells and CC tissues that express the protein. The protein activity in cells and CC useful in gene therapy. The gene encoding the protein of the invention may also be useful in gene therapy. The gene encoding the protein of the invention may also CC represents the human kinase amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human kinase protein, useful for treating or diagnosing disorders associated with an absence of, inappropriate, or unwanted expression the protein, e.g. inflammation or cancer, in drug screening assays and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; antiinflammatory; antipsoriatic; gene therapy; protein kinase; drug screening assay; tissue typing; chromosome 15; pharmacogenomic analysis; inflammation; cancer; leukaemia; lung tum kidney tumour; stomach adenocarcinoma; arteriosclerosis; psoriasis.
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06-DEC-2001; 2001US-00003295.
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                                   New human kinase peptides, useful for preparing a composition treating a disease or condition mediated by human kinases.
                                                              WPI; 2004-282461/26.
N-PSDB; ADM28580, ADM28582
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                                                                                                                                                                                                                                 gene therapy;
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 The invention relates
                   Claim 1; SEQ
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                                                                                                                                                                                              US2004063130-A1
                                                                                                                                                                                                                                                    Human proto-oncogene tyrosine kinase
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Query Match 100.0%; Score 3879; DB 8; Best Local Similarity 100.0%; Pred. No. 6e-280; Matches 752; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase peptide or its allelic variant, orthologue or fragment. The peptide is useful for preparing a composition for treating a disease or condition mediated by a human kinase protein e.g. cancer. The present sequence represents the amino acid sequence of the human proto-oncogene
                                                                                                                                                                                                 MEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPE
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RLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
                                                                                           ALNYGRYSSESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVF
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                                                                    ALMYGRYSSESDVWSFGILLWETFSLGASPYPMLSNQQTREFVEKGGRLPCPELCPDAVF
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Human homologue

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feline sarcoma

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Query Match
Best Local Similarity
Matches 752; Conser
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oncogene tyrosine kinase (poTK). The poTK polynucleotides and protein may
be used in the prevention, diagnosis and treatment of diseases associated
with inappropriate poTK expression, such as lung and kidney tumours,
leukenia and stomach adenocarcinoma. poTK may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of poTK by expressing
inactive proteins or to supplement the patients own production of poTK.
The encoded poTK may be used as an antigen in the production of
antibodies against poTK and in assays to identify modulators of poTK
expression and activity. The anti-poTK antibodies and antagonists may be
used to down regulate expression and activity and as diagnostic agents
for detecting the presence of poTK in samples. The present sequence
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ion, diagnosis and
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91.5%;
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d treatment of e.g. leukemia and
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                 CPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR 752
                                                                QVPVKWTAPEALNYGRYSSESDVWSFGILLWEIFSLGASPYPNLSNQQTREFVEKGGRLP
                                                                                                                  LQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLR
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XX Ho 24-JAN-2003 ABB99047 standard; (first entry) protein; 822 ξ

Human kinase related amino acid sequence

Human; kinase; proto-oncogene tyrosine kinase; antiarteriosclerotic; cytostatic; antiinflammatory; antipsoriatic; gene therapy; protein kinase; drug screening assay; tissue typing; chromosome 15; pharmacogenomic analysis; inflammation; cancer; leukaemia; lung tumo tumour; stomach adenocarcinoma; arteriosclerosis; psoriasis. tumours;

Homo sapiens.

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WO200277191-A2

03-OCT-2002.

27-MAR-2002; 2002WO-US009325

27-MAR-2001; 06-DEC-2001; 2001US-00817180 2001US-00003295

(PEKE) PΕ CORP NY.

ξ Ye Ģ Di Francesco ۲, Beasley 照.

WPI; 2003-029927/02

New human kinase protein, useful for treating or diagnosing disorders associated with an absence of, inappropriate, or unwanted expression the protein, e.g. inflammation or cancer, in drug screening assays and pharmacogenomics. xpression of assays and

Disclosure; Page 74-75; 75pp; English ð 밁 S 밁 5 밁 S 밁 5 밁

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CC The invention relates to a newly isolated peptide sequence of a human CC kinase that is related to the proto-oncogene tyrosine kinase subfamily. CC The activity of the kinase of the invention may be described as, CC cytostatic, antiarteriosclerotic, antiinflammatory and antipsoriatic. CC Peptides of the invention are useful in assays to determine the CC biological activity of the protein, in drug screening assays, tissue CC typing and pharmacogenomic analysis. They are also useful in treating or CC unwanted expression of the protein, such as inflammation, cancer (e.g. CC leukaemia, lung tumours, kidney tumours or stomach adenocarcinoma). CC arteriosclerosis, and psoriasis. Nucleic acid molecules of the invention CC assays. The specide and nucleic acid sequences are useful as models for the development of human therapeutic targets, aid in the identification CC the development of human therapeutic targets, aid in the identification CC therapeutic proteins and serve as targets for the development of human therapeutic targets for the development of human therapeutic targets for the development of human consequence are useful and concent of the invention may also be useful in gene therapy. The gene encoding the protein of the invention for the invention may also be useful an amino acid sequence relative to the human kinase sequence of the invention. NOTE: This sequence is not further mentioned in the continuation the invention. NOTE: This sequence is not further mentioned in the
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                                                                                                                                                                                                                            LVRESQGKQEYVLSVLWDGLPRHFIIQSLDNLYRLEGEGFPSIPLLIDHLLSTQQPLTKK
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KAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTL
                             KAKFLQEARILKQYSHPNIVRLIGVCTQKQPIXIVMBLVQGGDFLTFLRTEGARLRVKTL
                                                                                                           SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL
                                                                                                                                              SGVVLHRAVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDL
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ilarity 91.5%;
Conservative
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Pred. No. 1.5e-276;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human kinase peptides, useful for preparing a composition treating a disease or condition mediated by human kinases.
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06-DEC-2001; 2001US-00003295.
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 822 AA;
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Pred. No. 1.5e-276;
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                                                                            18-APR-2000;
26-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                 Novel human secreted
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                                                                                                                                   16-APR-2001; 2001WO-US008656
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                                       (HYSE-) HYSEQ INC
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2001US-00770160.
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WPI; 2001-611725/70

vaccination, acids encoding a range of human polypeptides, useful in genetic therapy.

Claim 20; Page 645-646; 765pp; English

The invention relates to novel human secreted polypeptides. The colypeptides and antibodies to the polypeptides are useful for certaining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a thereactions of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins care useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell croliferation; as anti-inflammatory agents; and in bone, cartilage, tendon at alor nerve tissue growth or regeneration; immune suppression and/or extinulation; as anti-inflammatory agents; and in treatment of leukaemias. CC satimulation; as anti-inflammatory agents; and in treatment of leukaemias. CC secreted proteins of the invention

Sequence 2202 AA;

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Pred. No. 3.4e-272;
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                                                                                                                                                             New human kinases and phosphatases (KPP) for preventing diseases or conditions associated e.g. cancer, acquired immunodeficiency syndro
                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2003; 2003US-0449059P.
19-MAR-2003; 2003US-0456932P.
28-MAR-2003; 2003US-0458844P.
09-APR-2003; 2003US-0461678P.
17-APR-2003; 2003US-0463937P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; kinase and phosphatase protein; KPP; enzyme; cytostatic; antiarteriosclerotic; anticrovalsant; nootropic; neuroprotective; cerebroprotective; anti-HV; antiallergic; antinflammatory; thyromimetic; gene therapy; cell proliferative disorder; cancer; thyromimetic; gene therapy; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
The present sequence represents the human kinase and phosphatase proceed (KPP), designated KPP-43. The human KPP sequences from the present invention have cytostatic, antiarteriosclerotic, anticonvulsant, neuroprotective, cerebroprotective, anti-HIV, antiallerg antiinflammatory and thyromimetic activities, and can be used in ge
                                                                                                                           Claim
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Gorvad AE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy. The human KPP proteins and polynucleotides can be used in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of KPP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. allergies) and developmental (e.g. Hypothyroidism, Cushing's Syndrome) disorders, or infections. They can also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of KPP. The KPP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide.
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Best Local Similarity
Matches 677; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for inducing neutralisation of cells or tissues by using a protein binding to CRAM (collapsing response mediator protein-associated molecule) protein or its encoded gene. The proteins and their encoded genes are useful in gene therapy and regenerative medicine, e.g. by inducing neutralisation of mitochondria. They are also applicable in diagnosis, drug development for neural diseases and spulcable in diagnosis for generative medicine in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes and proteins participating in neutralization of cells or tissues, useful in gene therapy and regeneration medicine, applicable in diagnosis, drug development for neural diseases and study of mechanism
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Nucleic acids encoding a range of vaccination, testing and therapy.
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                                 human polypeptides, useful
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Claim
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645; 765pp; English.
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The invention relates to novel human secreted polypeptides: The CC polypeptides and antibodies to the polypeptides are useful for CC determining the presence of or predisposition to a disease associated CC with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells CC expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or CC physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins CC are useful in genetic vaccination, testing and therapy, and can be used CC as nutritional supplements. They may be used to increase stem cell composition to regulate haematopoissis; and in bone, cartilage, tendon CC and/or nerve tissue growth or regeneration; immune suppression and/or CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias. CC AAU29510-AAU3304 represent the amino acid sequences of novel human creates.

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                                                                                                                                                                                             VFSGRLRADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYI
                                                                                                                                                                                                                                                                           SPALQNLYRLEGEGFPSIPLLIDHLLSTQQPLTKKSGVVLHRAVPKDKWVLNHEDLVLGE
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QSIRKRHR 752
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                                     SLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQEL
                                                      SLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQEL
                                                                                    NVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETF
                                                                                               NVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYSSESDVWSFGILLWETF
                                                                                                                                               VMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEK
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73.1%;
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Pred. No. 1.6e-169;
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밁 620 QSIRKRHR 627

ADK71829 standard; protein; 472 AA

ADK71829;

20-MAY-2004 (first entry)

Human kinase and phosphatase KPP-6 protein.

human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV; antiallergic; antiasthmatic; immunosuppressive; antithyroid; dermatological; antidásbetic; nephrotropic; antigout; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antipsoriatic; antiparaktinsonian; nootropic; anticonvulsant; hepatotropic; antipsoriatic; hemostatic; crocatatic; antilpaemic; antiparastic; antihelmintic; antibacterial; virucide; protozoacide; fungicide; cardiovascular disease; immune system; neurological; growth; development; cell proliferation; viral; bacterial; fungal; parastic; protozoan; helminthic infection; transgenic; gene therapy; enzyme; single nucleotide polymorphism; SNP.

WO2004018641-A2

04-MAR-2004.

25-AUG-2003; 2003WO-US026635.

26-AUG-2002; 2002US-0406172P. 25-SEP-2002; 2002US-041391DP. 27-SEP-2002; 2002US-0414296P. 11-OCT-2002; 2002US-0417821P.

(INCY-) INCYTE CORP

Chang H Chawla Baughn Becha ynn MR, Richardson Tha SD, Emerling BM, 1g H, Yang YG, Lee S la NK, Ramkumar J, 1g e J; n TW, Marquis JP, Swa M, Jin P, Wilson AD, ee SY, Khare R, Bllio J, Gururajan R, Tribo , Swarnakar A, Tang YT; n AD, Yue H, Gietzen KJ; Elliott VS, Hafalia AJA; Tribouley CM, Chien D, Tran

N-PSDB; 2004-226830/21. DB; ADK71888.

New human kinases and phosphatases, useful for diagnosing, treating preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, car cancer

Claim 1; ID NO 6 347pp; English

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ADK71829
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AC AD The invention relates to a novel isolated polypeptide which is a human CC kinase and phosphatase (KPP). The polypeptide of the invention CC demonstrates cardiovascular, antiarteriosclerotic, hypotensive, CC vasotropic, antiinflammatory, antianginal, anti-HIV, antiallergic, antiatsthmatic, immunosuppressive, antithyroid, dermatological, antiatsthmatic, immunosuppressive, antithyroid, dermatological, antirheumatic, antiparatingout, gastrointestinal, neuroprotective, CC antiparkinsonian, mootropic, antigout, gastrointestinal, neuroprotective, CC antiparkinsonian, mootropic, antitonvulsant, hepatotropic, antipsoriatic, CC antiparkinsonian, mootropic, antilpaemic, antiparasitic, antiphemitic, antiparasitic,
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XX ADL71
XX OBtec
XW OBtec
XW OBtec
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Best Local Similarity
Matches 411; Conser
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                                                                                               16-APR-2002; 2002JP-00113908
19-APR-2002; 2002US-0373594P
                                                                                                                                                                                                      Osteopathic; antiinflammatory; antirheumatic; antiarthritic; gene therapy; type II collagen; expression; cartilage disease; osteoarthritis; cartilage defect; rheumatoid arthritis; human.
                                                                                                                           16-APR-2003;
                                                                                                                                                23-OCT-2003
                                                                                                                                                                  WO2003087375-A1
                                                                                                                                                                                                                                            Type II collagen expression
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                              N-PSDB;
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purified protein that pr
preventing and treating
                            2003-845331/78.
DB; ADL71054.
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                                                         Honda G,
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promotes type
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Pred. No. 8
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II collagen expression, usefu disease, e.g. osteoarthritis,
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The invention relates to a purified protein (I) that promotes type II collagen expression. Also disclosed is an isolated polynucleotide encoding (I), a recombinant vector comprising the polynucleotide and a gene therapeutic agent comprising the recombinant vector as an active ingredient. The proteins, genes, agents and methods are useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis. The current sequence represents a human protein that promotes type II collagen expression.
                                                           Sequence
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Query Match
Best Local Similarity 45.5
Matches 376; Conservative
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                                              SSS-GLKQIPIKWTAPEALNYGRYSSESDVWSFGILLWETFSLGVCPYPGMTNQQAREQV
                                                                 AASGGLRQVPVKWTAPSALNYGRYSSSSDWSFGILLWETFSLGASPYDNSNQQTREFV
                                                                                                                        VLQEALQGLQVALCSQAKLQAQQELLQTKLEHLGPGEPPPVLLLQDDRHSTSSSEQEREG
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                                                                                                                                                                  EDLPQELKIKFLQEAKILKQYDHPNIVKLIGVCTQRQPVYIIMELVSGGDFLTFLRRKKD
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45.5%; Pred. No. 6.1e-129;
tive 150; Mismatches 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.1%; Score 1826.5; DB 7; Best Local Similarity 45.5%; Pred. No. 5.8e-127; Matches 376; Conservative 147; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a purified protein (I) that promotes type II collagen expression. Also disclosed is an isolated polynucleotide encoding (I), a recombinant vector comprising the polynucleotide and a gene therapeutic agent comprising the recombinant vector as an active ingredient. The proteins, genes, agents and methods are useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis. The current sequence represents a human protein that promotes type II collagen expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 823 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 46; 271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified protein that promotes type II collagen expression, useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis.
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19-APR-2002; 2002US-0373594P
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   EVVAIHREMAAAARIQPEAEYQGFLRQYGSAPDVPPCVTFDESLLEEGEPLEPGELQLN 299
                                                              HMLHNQYVLALKGAQLHQSQYYDTTLPLLLDSVQKMQEEMIKALKGIFDDYSQITSLVTE
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                                                                                                                   FAHHNRYVLGVRAAQLHHQHHHQLLLPGLLRSLQDLHEEMACILKEILQEYLEISSLVQD
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   Disclosure; Col 271-274; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                           Predicting the folded structure of proteins
                                                                                                                      WPI; 1999-570766/48.
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Best Local Similarity
Matches 262; Conserv
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   Predicting the folded structure of proteins
                                                                                                                                                                                                                                                                                                                                  25-MAR-1992;
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                                                                                                                                                                                                    (BENN/) BENNER
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Disclosure; Col 275-276; 113pp; English
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Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for understanding the interaction of a protein with other molecules. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 262 Ş.

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                                                          SESDVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVFRLMEQCWA 728
                                                                                                        CIHRDLAARNCLYTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYS
                                                                                                                                                       IVRLIGVCTQKQPIYIVMELVQGGDFLTFLRTEGARLRVKTLLQMVGDAAAGMEYLESKC
                                                                                                                                                                                         EDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDIKAKFLQEAKILKQYSHPN
                                                                                                                                                                                                     EDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDLKAKFLQEARILKQYSHPN
                      YEPGORPSFSTIYOELQSIRKRH 751
                                            CIHRDLAARNCLVTEKNVLKISDFGMSREEADGIYAAS
                                                                                                                                          IVRLIGVCTOKOPIYIVMELVQGGDFLTFLRTEGARLRMKTLLQMVGDAAAGMEYLESKC
YEPGORPSFSAIYQELQSIRKRH
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                 34.8%;
                                                                                                                                                                                                                                   Score 1350.5; DB 2;
Pred. No. 3.5e-92;
4; Mismatches 1;
                                                                                                                                                                                                                                                            DB 2;
                                                                                            -GLROVPVKWTAPEALNYGRYS
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                                                                                                                   668
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Search completed: March Job time : 176 secs 18, 2005, 15:59:19

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Database
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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/ Cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq: *
/ Cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq: *
/ Cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq: *
/ Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq: *
/ Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq: *
/ Cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq: *
/ Cgn2_6/ptodata/2/pubpna/USO1A_PUBCOMB.seq: *
/ Cgn2_6/ptodata/2/pubpna/USO1A_PUBCOMB.seq: *
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o/ptodata/2/pubpna/US06_NEW_PUB.seq:*
o/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	BG	ID	Description
–	2256	100.0	2674	13	3 US-10-003-295-1	Sequence 1, Appli
N	2256	100.0		17	US-10-660-763-1	Sequence 1, Appli
ω	2023.4	89.7		16	US-10-240-965-256	Sequence 256, App
4	326.8	14.5		10	US-09-918-995-1503	Sequence 1503, Ap
տ	296.2	13.1		ø	US-09-948-802-5	Sequence 5, Appli
0	296.2	13.1		15	US-10-121-925-5	Sequence 5, Appli
7	271.6	12.0		17	US-10-280-576-19	Sequence 19, Appl
8	227.2	10.1		13	US-10-003-295-3	Sequence 3, Appli
9	227.2	10.1		17	US-10-660-763-3	Sequence 3, Appli
10	201.2	8.9		15	US-10-101-510-525	Sequence 525, App
1	198	8. 8		18	US-10-384-339C-1	Sequence 1, Appli

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
170.4	170.4	170.4	170.4	174.6	174.6	174.6	174.6	174.6	174.6	174.6	174.6	174.6	174.6	174.6	174.6	176.2	185.4	185.4	185.4	185.4	185.4	185.4	185.4	185.4	•	185.4	185.4	185.4	198	198	198	198
7.6	7.6	7.6		•	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.8				•				8.2	8.2		8.2		8.8	8.8		٠
1611	1611	1611	1611	4151	4151	4089	4089	3544	3416	3416	3416	3416	3030	1050	816	1518	3935	3921	3921	3921	3921	3921	3921	3921	3921	3921	3921	3042	3370	3370	3370	3370
19	18	18	18	16	14	18	17	14	17	17	15	œ	16	18	18	17	19	19	18	18	17	17	17	17	16	15	10	18	18	18	16	16
占	US-10-887-588-3	US-10-887-588-1	US-10-476-962-3	٩	US-10-161-803-52	US-10-620-052A-7	US-10-291-808-13	0-161-803-	US-10-305-720-1483	US-10-464-805-2	US-10-292-524-1	US-08-987-689A-1	US-10-325-430-8	US-10-377-268-4	US-10-377-268-3	-10-280-576-	US-10-897-711-1	US-10-616-403-5	US-10-473-974-223	0-648	-10-287-226-	-10-342-887-103	-10-172	US-10-366-288-1	-10-269	US-10-007-926A-222	US-09-921-406C-29	US-10-384-339C-2	US-10-473-974-219	US-10-776-827-82	US-10-210-120-19	US-10-354-358-101
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Appli	Appli	Appli	Appli	Appli	Appl		Appl	Appl	1483, Ap	Appli	Appli	ppli	Appli	Appli	Appli	Appl	Appli	Appli	223, App	Appli	319, App	16, Ap	1036, Ap	Appli		2, App	Appl	2, Appli), App	App1	Appl	., App

ALIGNMENTS

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APPLICANT: GAN, Weiniu et al.
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE OF INVENTION: THEREOF
FILE REFERENCE: CL001183DIV
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2674
TYPE: DNA
GRGANISM: Homo sapiens
US-10-003-295-1
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Publication No. US20020168741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                      Matches 2256;
121 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC
                                                             132 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT
                                                                                                   61 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCCAGCGGGTCAAGAGT 120
                                                                                                                                          72 ATGGGCTTCTCTGAGCTGTGCAGCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG
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100.0%; Pred. No. 0;
ative 0; Mismatches
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                                                                                                                                                                                                                        Indels
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	1201 CTCCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGCAGGAGGGAG
187	1141 CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGGAGCCCCCGCCTGTGCTG 1200
	1081 CAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGGCCAAGCTGCAGGCCCAG 1140
	1021 GAAGAGGAGAACACCCACCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCTG 1080
_	961 ACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAAT 1020
	901 CTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAGCTGGCTG
	841 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGGAGCTCCAGCTGAACGAG 900
	781 TACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTGTGTCACGTTC 840
	721 GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGCATCCAGCCTGAGGCTGAG 780
	661 TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGAG 720
	601 CACCAGCTCCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGCT 660
	541 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGGCTGCGCAGCTACACCACCACCACCAC 600
	481 AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT 540
	421 CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAG
	361 CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC 420
	301 AAGCTGAGCCTGGTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG 360
	181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCCTGGGCTGAGATCACCAGCCAAACT 240
	192 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 251

292 TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCG
221 TACCAGGAGCTGCAGAGCATCCGAAAGCGGC
232
STTTG
2112 TGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGA
SACCTTCAGCCTGGGGGCCTCC
2052 GCCCTTAACTACGGCGGCTACTCCTCGAAAAGCGACGTGTGGAGCTTTGG
992 GGGG1
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1932 GTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAG
872 ATGG
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1741 GAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATG
681 CCCATCT
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501 AACTTTGGCGAAGTG
1441 AAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGA
1381 CTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGC
1321 AACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCAITCCTTTGCTCAICGA
332 ACACCCACGCTGGAGATCCTTAAGAGCCAC
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RESULT 2 US-10-660-763-1 ; Sequence 1, Application US/10660763

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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOL183DIVI
CURRENT APPLICATION NUMBER: US/10/660,763
CURRENT APPLICATION NUMBER: US/10/660,763
CURRENT FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2674
TYPE: DNA
ORGANISM: Homo Bapiens
US-10-660-763-1
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                                                                                   TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGAG
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080 GCAAGAAGCACTGCAGGGGCT	Оу	vati TCTT	Qy Ma
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960 CACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAA 1019 	Qy Db	OCHGANISM: HOMO BADIENB FEATURE: NAME/KEY: misc_feature OCHER INFORMATION: Incyte ID No. US20030165924A1 997347.6	; · · · · ·
900 GCTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAGCTGGCTG	Qy dd	SEQ ID NO 256 LENGTH: 2889 TYPE: DNA	S
840 CGATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGGAGCTCCAGCTGAACGA 899	Qy	PRIOR APPLICATION NUMBER: 60/195,106 PRIOR FILING DATE: 2000-04-05 PRIOR FILING DATE: 2000-04-05 PRIOR FILING DATE: 2000-04-05 PRIOR FILING DATE: 2000-04-05 PRIOR FILING DATE: 2000-04-05	
780 GTACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTGTGTCACGTT 839	Qy	TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION FILE REFERENCE: PA-0025 PCT CURRENT APPLICATION NUMBER: US/10/240,965	
720 GGTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCGCATCCAGCCTGAGGCTGA 779	Qy	APPLICANT: MANN, KICHAZO M. APPLICANT: SELLHAMER, Jeffrey J. APPLICANT: PORTER, Gordon J. APPLICANT: MIKITA, Thomas	ייייייי
660 TTGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGA 719	Qy Db	GENERAL INFORMATION: APPLICANT: INCYTE GENOMICS, INC. APPLICANT: SHIFFMAN, DOV APPLICANT: SOMOGYI, Roland APPLICANT: INCYTE GENOMICS	
600 CCACCAGCTCCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGC 659	Qy Db	WESULT 3 US-10-240-965-256 ; Sequence 256, Application US/10240965 ; Publication No. US20030165924A1	VS-1
540 TGCTCACCACAACCGCTATGTGCTGGGCGTGCGGGGCTGCGCAGCTACACCACCAGCACCA 599	Qy dd	2292 TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2327	D D
480 CAAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTT 539	og Vy	2232 AGGCTCATGGAGCAGTGCTGGGGCCTATGAGCCTTGGGCAGCGGCCCAGCTTCAGCACCATC 2291 2221 TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2256	dg dg
420 CCAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAGCGCAAGTACCAGGAGGCCAG 479	Qy Db	2172 GAGTTTGTGAGAAAGGGGGCCGTCTGCCCAGAGCTGTGTCCTGATGCCGTGTTC 2231 2161 AGCTCATGGAGCAGTGTGGGCTTGAGCCTGGGCAGCTTCAGCACCATC 2220	d dg
360 GCAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAG 419	Qy Db	2112 TGGGAGACCTTCAGCCTGGGGGGCCTCCCCCTATCCCAGCCTCAGCAATCAGCAGCAGCAGCG 2171 2101 GAGTTGTGGAGAGGGGGCCGTCTGCCCGCCCAGAGCTGTGCCTGATGCCGTGTTC 2160	y Qy dd
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181 CGGGCCATCAGCCCTGACAGCCCCCATCAGTCAGTCTGGGCTGAGATCACCAGCCAAACT 240	Q		σd

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CTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGA
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Sequence 5, Application US/09948802
Publication No. US20020172981A1
GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND

US-09-948-802-5

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Sequence 1503, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OF TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1503
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US-09-918-995-1503
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Best Local Similarity
Matches 328; Conserv
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OTHER INFORMATION: n =
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                  CGAAAGCGACGTGTGGAGCTTTGGCATCTT
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                                                           CAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTC
                                                                                      CAGACAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTC
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Pred. No. 3.9e-72;
0; Mismatches 2
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Sequence 5, Application US/10121925

| Publication No. US20030104505A1
| GENERAL INFORMATION: APPLICANT: ROBISON, KEITH E. APPLICANT: ROBISON, KEITH E. TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR FILE REPERENCE: MU1-090
| CURRENT APPLICATION NUMBER: US/10/121,925
| CURRENT FILING DATE: 2002-04-12
| PRIOR APPLICATION NUMBER: US/09/948,802
| PRIOR APPLICATION NUMBER: US/09/948,802
| PRIOR APPLICATION NUMBER: 09/387,212
| PRIOR FILING DATE: 1999-08-31
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: Patentin Ver. 2.0
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CURRENT APPLICATION NUMBER: US/09/948,802
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 5
LENGTH: 361
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US-10-121-925-5
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                                                                                SEQ ID NO 5
LENGTH: 361
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
Query Match
Best Local Similarity
Matches 333; Conserv
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ORGANISM: Homo sapiens
FEATURE:
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nes 333; Conserv
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 13.1%; ilarity 97.4%; Conservative
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Pred. No. 1.9e-64;
0; Mismatches 4;
 Score 296.2; DB 1
Pred. No. 1.9e-64;
0; Mismatches 4
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Best Local Similarity
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TYPE: DNA
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57.0%;
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RESULT 7

US-10-280-576-19

Sequence 19, Application US/10280576

Publication No. US20040044405A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: VASCULAR STENT OR GRAFT CO/
FILE REFERENCE: 09820.189

CURRENT APPLICATION NUMBER: US/10/280,576

CURRENT FILING DATE: 2002-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/343,732
PRIOR FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 25
SOPTWARE: PatentIn version 3.1
SEQ ID NO 19
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CAATACGATCATCCAAATATCGTAAAATTGATTGGCATTTGTGTGCAGAAGCAGCCCATC
                                                 CAGTACAGCCACCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATC
                                                                                                        CGAATGACCCTGCCCGACGAACAGAAGCGTAAATTCCTACAGGAAGGGCGCATCCTCAAG
                                                                                                                                            CGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGGATCCTGAAG
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Pred. No. 3.6e-58;
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Sequence 3. Application US/10003295
; Peublication No. US20020168741A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; SUTMARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-660-763-3
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Sublication No. US20040063130A1

GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: TREBEOF
TITLE OF INVENTION: TREBEOF
FILE REFERENCE: CL001183D1VII
CURRENT APPLICATION NUMBER: US/10/660,763
CURRENT APPLICATION OF 12

NUMBER OF SEQ ID NOS: 4
SOPTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 15207
                                                                                                                                                                                                                                                            Matches 394;
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCCAGCGGGTCAAGAGT
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                                                                 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC 2742
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                                                                                                                                                                                                                                                            Score 227.2; DB 17; Length 15297; Pred. No. 7.3e-47; O; Mismatches 8; Indels 152; Gaps
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US-10-101-510-525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEG ID NOS: 805
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 525
LENGTH: 3875
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 423; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
·10-101-510-525
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                                                      CGATCATGATCACCAGAATTTATGGAGAATGGAGCCCTGGATGCCTTCCTGAGGGAGC
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nilarity 54.9%;
Conservative
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Pred. No. 2e-40;
0; Mismatches 338;
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PRIOR APPLICATION NUMBER: DE 10100586.5
PRIOR FILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-10-26
PRIOR PILING DATE: 2001-10-26
PRIOR PILING DATE: 2001-10-26
PRIOR REPLICATION NUMBER: DE 10158411.3
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR PILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: Eph A1
; PATENT DOCUMENT NUMBER: NM00532
US-10-384-339C-1
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US-10-384-339C-1
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                                                                                                                           Matches 421;
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kreutzer, Roland
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 20200/2002
CURRENT APPLICATION NUMBER: US/10/384,339C
CURRENT FILING DATE: 2003-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/EP02/00152
PRIOR FILING DATE: 2002-01-09
                                                                                                                                                                                                                                                                                                                                      LENGTH: 2955
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      AAGTGTTCAGCGGACGCCTGCGAGCC------GACAACACCCTGGTGGCGGTGAAGT 1561
                                              GGGAGCTTGATCCAGCGTGGCTGATGGTGGACACTGTCATAGGAGAAGGAGAGTTTGGGG
                                                                            GGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCG
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                                                                                                                         8.8%;
nilarity 54.7%;
Conservative
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                                                                                                                             Score 198; DB 18;
Pred. No. 1.3e-39;
0; Mismatches 340;
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FILE REFERENCE: 689290-72

CURRENT APPLICATION NUMBER: US/09/967,768A

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US/60/236,109

PRIOR APPLICATION NUMBER: US/60/236,034

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,111

PRIOR PILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 325

SOFTWARE: PATENTIN VETSION 3.0

SEQ ID NO 144

LENGTH: 3370
                                                      ; LENGTH: 3370
; TYPE: DNA
; ORGANISM: HOMO 6
US-09-967-768A-144
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US-09-967-768A-144
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APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene
TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 144, Application US/09967768A Patent No. US20020150877A1
Query Match
Best Local Similarity
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APPLICANT: Hunter, John Joseph
APPLICANT: MacBeth, Kyle J.
APPLICANT: Teai, Fong-Ying
APPLICANT: Lesoon, Andrea
APPLICANT: Lightcap, Eric S.
APPLICANT: Milliamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Milliamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
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APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Milliamson, Marka A.
APPLICANT: Milliamson, Marka A.
APPLICANT: Milliamson, Andrea
APPLICANT: Hacker, S.
APPLICANT: Hacker, Applicant A.
APPLICANT: Lightcap A.
APPLICANT: Hacker, Applicant A.
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RESULT 13 US-10-354-358-101

Sequence 101, Application US/10354358 Publication No. US20030157082A1 GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals,

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TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943, TITLE OF INVENTION: 2150, 26583, 29011, 14031, 6178, 21225, 1420, 32236, 2099, TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES FILE REFERENCE: MPIOZ-02051RNOMMIM CURRENT FILING DATE: 2003-01-30 PRIOR APPLICATION NUMBER: US 60/354,358 CURRENT FILING DATE: 2002-01-31 PRIOR APPLICATION NUMBER: US 60/353,600 PRIOR APPLICATION NUMBER: US 60/364,517 PRIOR FILING DATE: 2002-03-15 PRIOR FILING DATE: 2002-03-15 PRIOR APPLICATION NUMBER: US 60/364,517 PRIOR FILING DATE: 2002-04-09 PRIOR APPLICATION NUMBER: US 60/371,075 PRIOR APPLICATION NUMBER: US 60/371,507 PRIOR APPLICATION NUMBER: US 60/371,507 PRIOR APPLICATION NUMBER: US 60/372,984 PRIOR APPLICATION NUMBER: US 60/372,984 PRIOR FILING DATE: 2002-04-19 PRIOR APPLICATION NUMBER: US 60/374,194 PRIOR APPLICATION NUMBER: US 60/382,995 PRIOR APPLICATION NUMBER: US 60/382,995 PRIOR APPLICATION NUMBER: US 60/382,995 PRIOR APPLICATION NUMBER: US 60/385,023 PRIOR FILING DATE: 2002-05-24 PRIOR FILING DATE: 2002-05-24 PRIOR FILING DATE: 2002-05-31 PRIOR APPLICATION NUMBER: US 60/388,853 PRIOR APPLICATION NUMBER: US 60/389,853 PRIOR APPLICATION
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SEQ ID NO 101
LENGTH: 3370
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PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (94)...(3048)
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TGAATCAAAACCTGTGCTGCAAGGTGTCTGACTTTGGCCTGACTCGCCTCCTGGATGACT
                                 TGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCCGAGAGGAAGCCGATG
                                                                                                       TGAACTACCTCAGTAATCACAATTATGTCCACCGGGACCTGGCTGCCAGAAACATCTTGG
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Pred. No. 1.3e-39;
0; Mismatches 340;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-19
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US-10-210-120-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
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Best Local Similarity
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TITLS OF INVENTION: Expression Profile of
FILE REFERENCE: UM-07221
CURRENT APPLICATION NUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
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GGGAGGACCAGCTGGTCCCTGGGCAGCTAGTGGCCATGCTGCAGGGCATAGCATCTGGCA
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No. US20030175736A1
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Pred. No. 1.3e-39;
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RESULT 15
US-10-776-827-82
; Sequence 82, Application US/10776827
; Publication No. US20040132086A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-776-827-82
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SOFTWARE: Patentin version 3.1
SEQ ID NO 82
LENGTH: 3370
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CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US/09/814,915
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2000-06-28
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APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
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TGGGCCAGTTTAGCCACCCGCATATTCTGCATCTGGAAGGCGTCGTCACAAAGCGAAAGC
                          TGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGC 1681
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US-09-949-016-628
US-09-949-016-628
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Sequence 1, Application US/09817180 | Sequence 1, Application US/09817180 | | Patent No. 6340584 | | GENERAL INFORMATION: GAN, Weiniu et al. | | TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES | | TITLE OF INVENTION: THEREOF | | FILE REFERENCE: CL001183 | | CURRENT APPLICATION NUMBER: US/09/817,180 | | CURRENT FILING DATE: 2001-03-27 | | NUMBER OF SEQ ID NOS: 4 | | SOFTWARE: FESTSEQ for Windows Version 4.0 | | SEQ ID NO 1 | | LENGTH: 2674 | | TYPE: DNA | | ORGANISM: Human | | US-09-817-180-1

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γ	1 ATGGGCTTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60
ŏ	72 ATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGTCCTGCAGCAAATGCAG 131
γ	61 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGA
ŏ	132 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT 191
¥	121 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 180
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¥	181 CGGGCCATCAGCCCTGACAGCCCCCATCAGTCAGTCCTGGGCTGAGATCACCCAGCCAAACT 240
ř	252 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT 311
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ř	312 GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC 371
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ř	372 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG 431
¥	361 CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC 420

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RESULT 2
US-10-003-295-1
US-10-003-295-1

Sequence 1, Application US/10003295

Patent No. 6886187

Patent No. 6886187

FARTHLINFORMATION:
APPLICANT: GAN, Weiniu et al.
APPLICANT: GNAIN WILL ET AL.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF

FILLE OF INVENTION: THEREOF

FILLE REFERENCE: CL001183DIV

CURRENT APPLICATION NUMBER: US/10/003,295

CURRENT FILING DATE: 2001-12-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FRASESEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2674

TYPE: DNA

ORGANISM: Homo Sapiens
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61 ACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAAT 1020	01 CTGACTGTGGAGAGCGTGAGCACACGCTGACCTCAGTGACAGATGAGCTGGCTG	41 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGAGCCTCCAGCTGAACGAG 900	781 TACCAAGGCTTCCTGCGACAGTATGGGTCCCACCTGACGTCCCACCCTGTGTCACGTTC 840	721 GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCGCATCCAGCCTGAGGCTGAG 780	661 TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGAG 720	601 CACCAGCTCCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGCT 660	541 GCTCACCACAACCGCTATGTGCTGGGCGTGCCGGGCTGCGCAGCTACACCACCAGCACCAC 600	481 AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT 540	421 CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAG	361 CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCCAGGACATTGAGAAGCTGAAGAGC 420	301 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG 360	241 GAGGGCCTGAGCCGCTTGCTGCGGCAGGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC 300	181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT 240 [121 GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 180	61 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT 120	1 ATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG 60	#Atch 100.0%; Score 2256; DB 4; Length 2674; cal Similarity 100:0%; Pred. No. 0;
8 B 8	B 성	99 QV	B 8	B 8	9 B 84	B &	B 2	B &	8 8	B 6	. B &	\$ \$ \$, B &	, B &	P 5	용 분 :	S B S
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                                                                                                                                                  RESULT 4
Sequence 5, Application US/09948802
Patent No. 6465232
GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH B.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR FILE REFERENCE: MNI-090
CURRENT APPLICATION NUMBER: US/09/948,802
CURRENT FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/387,212A CURRENT FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5 LENGTH: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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NUCLEIC ACID MOLECULES
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97.4%;
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Pred. No. 6e-56;
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Sequence 3, Application US/09817180

| Batent No. 6340584
| GENERAL INFORMATION:
| APPLICANT: GAN, Weiniu et al.
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTE
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: CL001183
| CURRENT APPLICATION NUMBER: US/09/817,180
| CURRENT FILING DATE: 2001-03-27
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: FRANCE OF WINDOWS Version 4.0
| SOFTWARE: FRANCE OF WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 361
; TYPPE: DNA
; CRGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurences of n indicate
US-09-948-802-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-817-180-3
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PRIOR FILING DATE: 199-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                            Matches 394; Conservative
                                                                                                                               Query Match
Best Local (
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Best Local :
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TYPE: DNA
                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                 Local Similarity
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61 GAGGCCGAGCTTCGTCTACTGGAGGGCCATGAGAAAGTGGATGGCCCCAGCGGGTCAAGAGT
                                                                         1 ATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG
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97.4%;
                                                                                                                               10.1%;
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                                                                                                          Score 227.2; DB 3;
Pred. No. 3.1e-40;
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Sequence 3, Application US/10003295

Patent No. 6686187

Patent No. 6686187

GENERAL INFORMATION:

APPLICANT: GAN, Weiniu et al.

ITILE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001183DIV

CURRENT FILING DATE: 2001-12-06

NUMBER OF SEQ ID NO.3: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO.3

LENGTH: 15297

TYPE: DNA

ORGANISM: Homo sapiens
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US-10-003-295-3
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Best Local Similarity
Matches 394; Conserv
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CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGGTGGGTCTCTATGGGACTCTGGTGGGT
                CGGGCCATCAGCCCTGACAGCCCCATCAGTC-----
                                                                             GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC
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ilarity 71.1%;
Conservative
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                                                                                                                                                                                                                                               Score 227.2; DB 4; Length 15297;
Pred. No. 3.1e-40;
0; Mismatches 8; Indels 152;
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US-09-949-016-12110
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Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENUTER, J. Craig et al.
TITLE OF INVERTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 12110
LENGTH: 19152
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Best Local Similarity 100.0%; Pred. No. 4.4e-37;
Matches 213; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                         CGGGCCATCAGCCCTGACAGCCCCCATCAGTCAG 213
                                                                                                    GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 180
                                                                                                                                                             GAGGCCGAGCTTCGTACTGGAGGGCATGAGAAAGTGGATGGCCCCAGCGGGTCAAGAGT
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RESULT 8 US-09-949-016-15795

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                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-82
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US-09-949-016-15795
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15795
LENGTH: 19153
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PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                       Sequence 82, Application US/09814915A Patent No. 6750015
                                                                       Query Match
Best Local Similarity
                                                                                                                                                               SEQ ID NO 82
LENGTH: 3370
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Best Local Similarity
                                                          Matches 421;
                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2000-06-28
                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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 GGGAGCTTGATCCAGCGTGGCTGATGGTGGACACTGTCATAGGAGAAGGAGAGTTTGGGG
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Pred. No. 4.4e-37;
                                                         Score 198; DB 4; ]
Pred. No. 5.2e-34;
0; Mismatches 340;
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US-09-949-016-628
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Patent No. 681233
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AGCTCATGAAGAACTGCTGGGCATATGACCGTGCCCGCCGGCCACACTTC
                                                       GGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTC
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 628
PRIOR FILING SEQ ID NO 628
LENGTH: 3921 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTEN: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14 ORGANISM: Human

THEREOF

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Sequence 2120, Application US/09949016

PALEAR NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITITE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CLOOL307

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 05/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

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PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08
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Best Local Similarity
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     SEQ ID NOS: 207012
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US-09-949-016-5662
; Sequence 5662, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
GENERAL INFORMATION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
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Best Local Similarity 55.1%;
Matches 385; Conservative
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; SOFTWARE: FastSEQ for Windows Version

; SEQ ID NO 2120

;. LENGTH: 3921

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-2120
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PLICATION NUMBER: 60/231,498
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.
SEC ID NO 5662
LENGTH: 3386
TYPE: DNA
ORGANISM: Human
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                                                                                                                                      RESULT 13
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                                                    Sequence 2, Application US/08357642A Patent No. 5837524 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.7%;
Best Local Similarity 54.7%;
Matches 392; Conservative
APPLICANT: Sima Lev
APPLICANT: Joseph Schlessinger
TITLE OF INVENTION: PYK2 RELATE
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  PYK2 RELATED PRODUCTS
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Pred. No. 7.5e-29;
0; Mismatches 319;
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; MOLECULE TYPE:
US-08-357-642A-2
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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1918 GATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCT
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392; Conserv
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                                                                CTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCC
                                                                                                   GCCATGGCCTACCTGGAGAGCATCAACTGCGTGCACAGGGACATTGCTGTCCGGAACATC
                                                                                                                                                                     CGGAACAAGAACTCCCTGAAGGTGCTCACCCTCGTGCTGTACTCACTGCAGATATGCAAA 1712
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                                 CTGGTGGCCTCCCCTGAGTGTGAAGCTGGGGGACTTTGGTCTTTCCCCGGTACATTGAG
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linear
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54.7%;
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Pred. No. 7.5e-29;
0; Mismatches 319;
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/357,642

APPLICATION NUMBER: 15,1994

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 21/12

TELECOMMUNICATION INFORMATION:
"TELECOMMUNICATION INFORMATION:
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                                                             Query Match
Best Local Similarity
Matches 392; Conserv
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                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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STREET: Suite 4..
CITY: Los Angeles
TMATE: California
U.S.A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
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APPLICATION NUMBER: US
FILING DATE: June 2, 1
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TITLE OF INVENTION: PYK-2 RELATED PRODUCTS
TITLE OF INVENTION: METHODS
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                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 355-0440
                                                                                                                                                                                                                                                     ENGTH:
1498 GGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCCTGGTGGCGGTG
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Conservative
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                                                                  Score 174.6; DB 2;
Pred. No. 7.5e-29;
0; Mismatches 319;
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                                                                                                            Length 3416;
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US-09-016-434-1483
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Patent No. 650093
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
    CLASSIFICATION:
                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                          CITY: PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGCCCACCTGGATCATCATGGAATTGTATCCCTATGGGGAGCTGGGCCCACTACCTGGAG
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3174 PORTER DRIVE
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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9988304
US-09-016-434-1483
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA.0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1483:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 392; Conserv
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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2158 TTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCAGCTTCAGC 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1476 AAGACCTGCAAGAAAGACTGCACTCTGGACAACAAGGAGAAGTTCATGAGCGAGGCAGTG
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                                                                          2010 ATCGGGGTGCTGGAGAAAGGAGACCGGCTGCCCAAGCCTGATCTCTGTCCACCGGTCCTT 2069
                                                                                                        CGGGAGTTTGTGGAGAAGGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTG 2157
                                                                                                                                                                                   CTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACA 2097
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                                                                                                                                                                                                                                                                                                                                          GAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTG 2037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGC 1857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGTGGCCTCCCCTGAGTGTGAAGCTGGGGGACTTTGGTCTTTCCCCGGTACATTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCATGGCCTACCTGGAGAGCATCAACTGCGTGCACAGGGACATTGCTGTCCGGAACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.7%; Score 174.6; DB 4; Length 3416; nilarity 54.7%; Pred. No. 7.5e-29; Conservative 0; Mismatches 319; Indels 6;
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TATACCCTCATGACCCGCTGCTGGGACTACGACCCCAGTGACCGGCCCCGCTTCACC 2126

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> Search completed: March 19, Job time: 373.746 secs 2005, 14:24:17

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115
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13179.075 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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475.6	494	496.6	497.6	498	506.4	515.8	517	526.2	528.4	547.2	551.2	570.2	570.8	574.4	574.8	575.8	581.6	587.6	597	599.4
21.1	21.9	22.0	22.1	22.1	22.4	22.9	22.9	23.3	23.4	24.3	24.4	25.3	25.3	25.5	25.5	25.5	25.8	26.0	26.5	26.6
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BG803019	BQ015500	BI910442	BE917487	BP256574	AW658298	CF731836	BX644743	BF159511	BP332887	CK943999	AW701492	CB990282	BM922603	BQ807439	BQ924403	CK357411	CK788677	BU191031	BQ712558	BQ679512
BG803019	BQ015500	BI910442	BE917487	BP256574	AW658298	CF731836	BX644743	BF159511	BP332887	CK943999	AW701492	CB990282	BM922603	BQ807439	BQ924403	CK357411	CK788677	BU191031	BQ712558	BQ679512
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ALIGNMENTS

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VERSION
KEYWORDS
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JOURNAL
REMARK
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Matches 2131; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                     source
32
                                 μ
                                                                                                                                                                                                                                                                                                                     Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2461)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR624741 2461 bp mRNA linear full-length cDNA clone CSODI069YK21 of Placenta Cot of Homo sapiens (human).
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HTC; CNSLT_cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Faraday Avenue
                     ATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 2461)
                                                                       Conservative
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO59YK21"
/tissue_type="Placenta_Cot_2
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                       1. .2461
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                       76.8%;
84.9%;
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                                                                     Score 1732.8;
Pred. No. 0;
0; Mismatches
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Query Natches Antiches Qy Db Qy Db	FEATURES SOURCE	TITLE JOURNAL COMMENT	JOURNAL REMARK REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE	RESULT 2 CR593957 LOCUS DEPINITION ACCESSION	р У	ያ <i>ያ</i>	B 8	B	Ş	дb
Query Match 44.4%; Score 1002; DB 3; Length 1189; Best Local Similarity 100.0%; Pred. No. 1.2e-200; Matches 1002; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1255 GGAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAG 1314	division of Invitrogen. Location/Qualifiers 11189 1. organism="Homo sapiens" /mol type="mRNA" /db_xref="taxon.9606" /clone="CSDI008Y607" /tissue type="placenta Cot 25-normalize/plasmid="pCMVSPORT_6"	Direct Submission Submitted (20-UUL-2004) Genoscope - Centre National de Sequenc Submitted (20-UUL-2004) Genoscope - Centre National de Sequenc Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cr : Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five end enriched, double-strand cDNA was digested with Not I and content into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Lik	Unpublished Contact: Feng Liang Email: f http://fulllength.invitrogen.c Faraday Avenue 2 (bases 1 to 1189) Genoscope.		CR593957 of Homo sapi CR593957	2207 GCTTCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAAAGCCGCATCGG 2256	2147 CTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGCCCA 2206	2087 ATCAGCAGACACGGGAGTTTGTGGAGAAAGGGGGGCCGTCTGCCCTGCCCAGAGCTGTGTC 2146	2278 2277	2027 TTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCCAACCTCAGCA 2086	
RESULT 3 BX356089 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	9	Q	8 B 8	D	B 9 B 9	Qy Db	B 8	B 8	망	Ş	Db
BX356089 BX356089 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODIO08YG07 5-PRIME, mRNA sequence. BX356089 BX356089.2 GI:46290249 EST. Homo sapiens (human) Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 936)	841 ACACGGGAGTTTGTGGAGAAGGGGGCCCCCCCCCCCCCC	721 CCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATC 780 2035 TTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTCAGCAATCAGCAG 2094	GCCGATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCA	1795 GCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGG	1675 AAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGCGACTTCCTGACCTTCCTC 1734	1615 AGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAG 1674	1555 GTGAAGTCTTGTCGAGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCG 1614	1495 CGGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCTGGTGGCG 1554.	181 GTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGA 240	1435 GTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTTGGGTGAGCAGATTGGA 1494	

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(Lingublished (2001)
(Dn May 5, 2003 this sequence version replaced gi:30372027.
(Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefggenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPRT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                       GCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAAC
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
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Nature 409, 685-690 (2001)
                                                                                                                                                Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3373)
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                                                                                   GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="lung"
/clone_Tib="RIKEN full-length enriched mouse
/dev_stage="adult"
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/db_xref="taxon:10090"
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/mol_type="mRNA"
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합 정 함 :	Query Match Best Local Matches 86	ORIGIN	FEATURES SOU		REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 5 AL542976 LOCUS DEFINITION	ъ 2	Q dd	QQ VQ	в 8
ATGGCTTCTCTCTAGCTGTGCAGCCATGAGAAAGTGGATGGCCCAGCGGTCAAAAGTGCAGAGCCGAGCCAAGAGTTCATCTCTCTAGCTGTGAGCATGAGAAAAGTGGATGGCCCAGCGGGTCAAAAGAGT	24	/tissue type="PLACENTA" /clone Tib="Homo sapiens PLACENTA" /clone Tib="Homo sapiens PLACENTA" /note="Vector: pCNVSPORT 6; 1st strand cDNA was primed /note-"Vector: pCNVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."	For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODEO13DH01QP1&c=7663.f. RES 1936 1936 yorganisms"Homo sapiens" /mol_type="mRNA" /db xrefs="taxon:9606" /cl Tenes"RODEN17402"	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7663.f	C 00	5-PRIME, mRNA sequence. N AL542976. AL542976.3 GI:45718543 EST. Homo sapiens (human) SM Homo sapiens	; S AL542976 AL542976 936 bp mRNA linear EST 24-MAR-2004 CON AL542976 Homo sapiens PLACENTA Homo sapiens CDNA clone CSODE013YP02	1305 CCGCCCAAGTTCTCGAACCTGTACCGACTGGA 1337	1245 GCGAGAGGGGGAAAGGACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTT 1304	1185 GCCCCGCCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCCTCGGAGCAGGA 1244	1125 CAAGCTGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCCGGCGA 1184
AUTHO TITLE JOURN COMMENT	SOURCE SOURCE ORGANIS	RESULT 6 BM456755 LOCUS DEFINITION ACCESSION VERSION	D & B &	9 Q D Q	8	D Q D	Q	, סמ אס	Db Q	Db Qy	D Qy
	N N	T 6 755 BM456755 TITION AGENCOURT 6403957 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:555 SION BM456755 BM456755.1 GI:18505795	### ##################################	61 16 21 76	541 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCACCACCACCACCACCACCACCACCACCACCACC	477 CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAG	361 CAGCAGCTGCAGGAGGTCACCAAGACCCACAGGCCAGGACATTGAGAAGCTGAAGAGC	301 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG	241 GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC	181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT	121 GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC

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FEATURES
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Plate: LLMN12347 row: b column: 05
High quality sequence stop: 704.
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/lab host="PH108 (phage-resistant)"
/clone_lib="NIH_MGC 92"
/note="Torgan: testis; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5583652"
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On May 5, 2003 this sequence version replaced Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO51BH10QP1&c=7663.f. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was dested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex -
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1 (bases 1 to 968)
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                                                                                                 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT
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/db_xref="taxon:9606"
/clone="CS0DI051Y020"
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95.9%;
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Mammalia; Eutheria; Primates; Catarrhini; Homi 1 (bases 1 to 939)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 8, 2003 this sequence version replaced Contact: Genoscope
                                                                                                                                             BX381726 BX381726 P39 bp mRNA linear BX381726 Homo sapiens PLACENTA COT 25 NORMALIZED F clone CSODIO69YK21 5-PRIME, mRNA sequence.
BX381726
                                                                                                Homo
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                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
            gi:30443719
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               ACACCAGCTCCTGCTGCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGC
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO69AF11QP1&c=7663.f. Location/Qualifiers
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-CACCAGCTCCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGACGAGGAGATGGC
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/db_xref="taxon:9606"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectonpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2516 row: o column: 07
High quality sequence stop: 610.
Location/Qualifiers
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Homo sapiens
                          AACTCAGGGCCCCTGAGCAAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAG 342
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                                                                                                                                         Conservative
                                                                                                                                                                                                                    /lab host="DH10B (phage-resistant)"
/clone_lib="NHH_MGC_113"
/clone_lib="NHH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: RecRI; cDNA made by oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubbin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301278"
                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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                                                                                                                                                    Score 771.6; DB 5;
Pred. No. 4.8e-152;
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 5, 2003 this sequence version replaced Contact: Genoscope
Genoscope - Centre National de Sequencage
                                                                                                   Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 980)
                                                                                                                                                                                     BX356088 980 bp mRNA linear BST 08-APR-200-BX356088 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODIO08YG07 3-PRIME, mRNA sequence.

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BX356088 2 GI:46288403
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CCGTCTGCCCTGCCCAGAGCTGTGTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTG
                                                                                  GGCCTCCCCTATCCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGG
                                                                                                                                                                                                 CTCCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGG
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                                                      GGCCTCCCCTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGARAAGGGGGG
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/Clone_Tib="HOmo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR.
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/clone="CSODI008YG07"
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Pred. No. 8.9e-148;
1; Mismatches 8;
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1 (bases 1 to 922)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
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922 bp mRNA linear EST 04-SEP-2002
AGENCOURT 8071250 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6090558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                        AGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACCACCACCATG
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/lab host="DH10B (phage-resistant)"
/clome libe"NIH MGC 112"
/clome libe"NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript I RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6090558"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1114)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                            TGCAGCTGCTGCCCGCATCCAGCCTGAGGCTGAGTACCAAGGCTTCCTGCGACAGTATGG
                                                                                                                             ATACCTGGAGATTAGCAGCCTGGTGCAGGATGAGGTGGTCGCCATTCACCGNGAGATGGC
                                                                                                                                                                                                 GCGGTCACTGCAGGACCTGCACGAGGAGATGGCTTGCATCCTGAAGGAGATCCTGCAGGA
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/db_xref="taxon:9606"
/clone="IMAGE:5589213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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Pred. No. 3.6e-139;
0; Mismatches 27;
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found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
Plate: LLMN12361 row: i column: 22
High quality sequence stop: 566.
                                                                              /clone_lib="NIH_MGC_125"
/note="Torgan: ovary (pool of 3); Vector: pCMV-SPORT6;
/note="Torgan: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: ECORV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(ECORV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
Length
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Indels

9

Gaps

6

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368

739

428

799

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859 488

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REFERENCE
AUTHORS
TITLE
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KEYWORDS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTp
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT_8071838 NIH_MGC_112 Homo sapiens 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 847)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                        AGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATG
                                                                                                                                                                                                                          TCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGCCAGTACCGAGCTCTGGCAC
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                                                                                                                                                                                            TCAGTCAGACCCACAGCAGGACATTGAGAAGCTGAAGAGCCAGTACCGAGCTCTGGCAC
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="melanotic melanoma, cell line"
/lab host="DH10B (phage resistant)"
/clone libs"NIH MGC 112"
/clone libs"NIH MGC 112"
/note="organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6088554"
                                                                                                                                                                                                                                                                                                     31.2%;
99.4%;
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                                                                                                                                                                                                                                                                                                     Score 703.2; DB 5;
Pred. No. 1.3e-137;
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TITLE
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1 (bases 1 to 989)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30376296.

Contact: Genoscope
                                                                                                                                                                                                            Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               989 bp mRNA linear EST 08-APR-200 BX359009 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI051Y020 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                   For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO51BH10NP1&c=7663.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI051Y020"
                                                                                                                               Location/Qualifiers
tissue_type="PLACENTA COT 25-NORMALIZED"/
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EST 08-APR-2004

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Query Match
Best Local Similarity
Matches 787; Conserv
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BX327963 973 bp mRNA linear EST 07-APR BX327963 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens clone CSODI069YK21 5-PRIME, mRNA sequence.
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/note="List strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR '
sites of the pCMVSPORT 6 vector. Library was normalized
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Pred. No. 2e-136;
3; Mismatches 13;
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Mammalia; Eutheria;
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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CCCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCTGCAAGAAGCACTGCAGGG 1097
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                                                                                                                        GCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAATGAAGAGGAGGAGAACACCCA
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/db_xref="taxon:9606"
/clone="CS0DI069YK21"
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Search completed: March 19, 2005, 14:10:46 Job time : 6521.86 secs	661 TCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCCAGTTCTCG 704	1277 TCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTCG 1320	601 CCACTCCACGTCCTCGGACAGGNAGCGAGAGGGNGGGAAGGACACCCACGCTGGAGA 660	1218 CCACTCCACGTCCTCCTCGGAGCAGGAGGAGGG-GGGAAGGACACCCCACGCTGGAGA 1276	541 CAAGCTGGAGCACCTGGGCCCCGGCGAGCCCCCGCCTGTGCTGCTCCTGCAGGATGACCG 600	1158 CAAGCTGGAGCACCTGGGCCCGGCGGGGAGCCCCCGCCTGTGCTGCTCCTGCAGGATGACCG 1217	481 GCTGCAGGTAGCGCTGTGCAGCCAGGCCAAGCTGCAGGCCCAGCAGGAGTTGCTGCAGAC 540	1098 GCTGCAGGTAGCGCTGTGCAGGCCAGGCCAAGCTGCAGGCCCAGGAGTTGCTGCAGAC 1157

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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ABV75413
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         Aba94500 Human pro
Abv75413 Human kin
Adm28580 Human pro
Adk71888 Human kin
Aa895001 Human DNA
Addr39816 Human kin
Aa895001 Fes/fps p
Add171052 Gene enco
Add74298 Novel can
Add71052 Gene enco
Add64298 Novel can
Add71054 Gene enco
Add64298 Novel more
Add71054 Human pro
Abx14976 Human pro
Abx14976 Human pro
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Acc57665 Drosophil
Ab114457 Drosophil
Ab114457 Drosophil
Ab114457 Drosophil
Ab114457 Drosophil
Ab114457 Drosophil
Ab11457 Drosophil
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185.4	185.4	185.4	185.4	185.4	185.4	185.4	185.4	185.4	198	198	198	198	198	198	198	198	198	198	199.2	199.6		201.2	225.6	227.2
	8.2	8.2	8.2	8.2	8.2	8.2	8.2	8 .2	8 8	8.8	8 8	8.8	8.8	8 8	8.8	8 8	8.8	8.8	8.8	8.8	8.9	8.9	10.0	10.1
3921	3921	3921	3919	3346	3042	3042	3042	3042	3370	3370	3370	3370	3370	3370	2955	2955	2955	2955	2778	5616	3875	3286	12263	15297
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ADB37439	ABZ34865	ABV94231	ACN37278	ACN42099	ABL91659	ABX09937	ABZ35694	ABV78118	ADQ80244	ADJ75094	ADE38440	ADD18447	ABZ34861	ABL67952	ABL91658	ABX09936	ABZ35693	ABV78117	ADP28218	ADE08824	ABZ35414	ADK71885	ABK84514	ADM28582
Adb37439 Human can	Abz34865 Coding se	Abv94231 Breast ca	Acn37278 Tumour-as	Acn42099 Human dia	Abl91659 Human pol	Abx09937 Human eph	Abz35694 Human eph		Eph1 cf	Adj75094 Marker ge	Ade38440 Human pro	Add18447 Human pro	Abz34861 Coding se	Abl67952 Ovary can	Abl91658 Human pol	Human	Abz35693 Human eph	Abv78117 Human eph	Adp28218 Human sec	Ade08824 Novel DNA	Abz35414 Human gen	Adk71885 Human kin	Abk84514 Human cDN	Adm28582 Human pro

ALIGNMENTS

RESULT 1

ABA94500 standard; cDNA; 2674 BP

ABA94500;

09-APR-2002 (first entry)

Human proto-oncogene tyrosine kinase encoding cDNA.

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3'UTR
                                                                                                                                                                                                                         5'UTR
                                                                                                                                                                                                                                                                    Proto-oncogene tyrosine kinase; poTK; tumour; cytostatic; anti-leukemic; gene therapy; protein therapy; vaccine; enzymatic-inhibition; human; anti-kinase; ss.
       Nucleic acids encoding a proto-oncogene tyrosine kinase, useful for the prevention, diagnosis and treatment of e.g. leukemia and lung tumors.
                                 WPI; 2002-138497/18.
P-PSDB; ABB07354.
                                                            Gan W,
                                                                                                                                                                                                                                                    Homo sapiens.
                                                                              (PEKE ) PE CORP NY.
                                                                                               27-MAR-2001; 2001US-00817180
                                                                                                                27-MAR-2001; 2001US-00817180
                                                                                                                                  22-JAN-2002.
                                                                                                                                                   US6340584-B1.
                                                            Ye J, Di Francesco V,
                                                                                                                                                                    /*tag= a
72. 2330
/*tag= /
/*tag= a
/product= "proto-oncogene tyrosine kinase"
2331. .2674
                                                                                                                                                                                                                                  Location/Qualifiers
                                                            Beasley
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CC The invention provides isolated nucleic acid sequences encoding a protococogene tyrosine kinase (poTK). The poTK polynucleotides and protein may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate poTK expression, such as lung and kidney tumours, compared with decreased expression, such as lung and kidney tumours, compared with decreased expression by rectifying mutations or deletions compared in a patient's genome that affect the activity of poTK by expressing compared in a patient poTK may be used as an antigen in the production of poTK. The encoded poTK may be used as an antigen in the production of poTK. CC The encoded poTK may be used as an antigen in the production of compared in a patient poTK and in assays to identify modulators of poTK. Expression and activity and as diagnostic agents cor detecting the presence of poTK antibodies and antagonists may be used to down regulate expression and activity and as diagnostic agents cor detecting the presence of poTK in samples. The present sequence cor represents a cDNA encoding the human poTK some potential sequence 2674 BB; 662 A; 767 C; 810 G; 435 T; 0 U; 0 Other; Best Local Similarity 100.0%; Score 2256; DB 6; Length 2674; Best Local Similarity 100.0%; Score 2256; DB 6; Length 2674; Matches 2256; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2256; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2256; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2256; DB 6; Length 267AAATGCAG 60
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672 421 432 361 372 301 241 252 181 192 121 661 601 541 481 492 721 61 72 GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCGCATCCAGCCTGAGGCTGAG CACCAGCTCCTGCTGCCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGCT GCTCACCACAACCGCTATGTGCTGGGGGTGCGGGCTGCGCAGCTACACCACCACCACCAC CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC CGGGCCATCAGCCCTGACAGCCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGAG TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGAG GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCACCACCACCAC AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCCAAGCGCAAGTACCAGGAGGCCAGC CAGCAGCTGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC 191 60 131 540 551 420 360 300 240 251 180 731 660 671 600 611 480 491 431 311 791 0

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CTGAGCACCCAGCAGCCCCTCACCAAGAAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCC

AAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGTGAGCAGATTGGACGGGGG

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GAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCTGGC

GAGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCTGGC

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CCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGGGACTTCCTGACCTTCCTCCGCACG

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1620 1691 1680

CTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAG

CTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAG

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TCTTGTCGAGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATC

TCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATC

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AACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAACACCCCTGGTGGCGGTGAAG

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1321 AACCTGTACCGACTGGAAGGGGGAAGGCTTTCCTAGCATTCCTTTGCTCATCGACCACCTA
1332 ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTCG
1261 ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCGGCCCCAAGTTCTCG
1272 CTCCTGCAGGATGACCGCCACTCCACGTCCTCGGAGCAGGAGCGAGAGGGGGGAAGG
1201 CTCCTGCAGGATGACCGCCACTCCACGTCCTCGGAGCGAGC
1212 CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGGGAGCCCCCGCCTGTGCTG
1141 CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCCGAGCCCCCGCCTGTGCTG
1152 CAAGAAGCACTGCAGGGCTGCAGGTAGCGCTGTGCAGCCAAGCCGAAGCTGCAGGCCCAG
1081 CAAGAAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCCAGGCCAAGCTGCAGGCCCAG
1092 GAAGAGGAGAACACCCACCCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGGCAAGTGCTG
1021 GAAGAGGAGAACACCCCACCCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCTG
1032 ACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAAT
961 ACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAAT
972 CTGACTGTGGAGAGCGTGCAGCACACGCTGAGTGACAGATGAGCTGGCTG
901 CTGACTGTGGAAAAGCGTGCAGCACACGCTGACCTCAGTGACCAGATGAGCTGGCTG
912 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCCAGCTGAACGAG
841 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCCAGCTGAACGAG
852 TACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGCTCCCACCCTGTGTCACGTTC
781 TACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTGTGTCACGTTC
792 GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCCCGCATCCAGCCTGAGGCTGAG

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WPI; 2003-029927/
P-PSDB; ABB99046.
                                                                                                                                                                                                                                                                                                                Human; kinase; proto-oncogene tyrosine kinase; antiarteriosclerotic; cytosteatic; antiinflammatory; antipsoriatic; gene therapy; protein kinase; drug screening assay; tissue typing; chromosome 15; pharmacogenomic analysis; inflammation; cancer; leukaemia; lung tumours; kidney tumour; stomach adenocarcinoma; arteriosclerosis; psoriasis; gene;
                                                                                27-MAR-2001; 2001US-00817180
06-DEC-2001; 2001US-00003295
                                                                                                                                                                                              3'UIR
                                                                                                                                                                                                                                                     5'UTR
                                                                                                                                                                                                                                                                                                                                                                                      Human kinase encoding cDNA.
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/product= "protein kinase"
2331. .2674
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New human kinase protein, useful for treating or diagnosing disorders associated with an absence of, inappropriate, or unwanted expression of the protein, e.g. inflammation or cancer, in drug screening assays and pharmacogenomics.

Claim 4 (b); Fig 1; 75pp; English.

The invention relates to a newly isolated peptide sequence of a human CC kinase that is related to the proto-oncogene tyrosine kinase subfamily. CC The activity of the kinase of the invention may be described as, CC cytostatic, antiarteriosclerotic, antiinflammatory and antipsoriatic. CC peptides of the invention are useful in assays to determine the CC peptides of the invention are useful in assays to determine the CC peptides of the invention are useful in assays to determine the CC diagnosing disorders characterised by an absence of, inappropriate, or CC unwanted expression of the protein, such as inflammation, cancer (e.g. CC leukaemia, lung tumours, kidney tumours or stomach adenocarcinoma), CC arteriosclerosis, and psoriasis. Nucleic acid molecules of the invention CC are useful as probes, primers and chemical intermediates in biological cassays. The peptide and nucleic acid sequences are useful as models for the development of human therapeutic targets, and in the identification CC therapeutic agents that modulate kinase protein activity in cells and CC tissues that express the protein. The protein of the invention may also be useful in gene therapy. The gene encoding the protein of the invention CC consecuted to human chromosome 15. The current sequence the human kinase encoding CDNA

Sequence 2674 BP; 662 A; 767 C; 810 G; 435 T; 0 U; 0 Other;

S 밁 δ 밁 S 밁 S S 밁 S á ð S 몽 밁 S Query Match Best Local Similarity Matches 2256; Conserv 541 481 492 421 432 361 372 301 312 241 252 181 192 132 121 61 72 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCACCACCACCAC AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG GACAGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAGTGGATGGCCCAGCGGGTCAAGAGT ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG AAAGACAAGGACCGTGACAAGGCCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC GAGGGCCTGAGCCGCTTGCTGCGGCAGCACCACGAGAGGATCTGAACTCAGGGCCCCTGAGC CGGGCCATCAGCCCTGACAGCCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT CGGGCCATCAGCCCTGACAGCCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCCAGCGGGTCAAGAGT ATGGGCTTCTCTGTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC **AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG** GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCTGAGC Conservative 100.0%; 0 Score 2256; Pred. No. 0; Mismatches B 0 8 Length 2674; Indels 0 Gaps 611 600 540 551 480 491 420 431 360 371 300 311 240 251 180 191 120 131 60

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Human proto-oncogene tyrosine kinase cDNA.
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Query Match
Best Local Similarity
Matches 2256; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4;
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                 26-AUG-2002;
25-SEP-2002;
27-SEP-2002;
11-OCT-2002;
                                                                                                                                                                                                                                                                                               human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV; antiallergic; antiasthmatic; immunosuppressive; antithyroid; dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic; antipsoriatic; hemostatic; cytostatic; antilipaemic; antiparasitic; antibelmintic; antibacterial; virucide; protozoacide; fungicide; cardiovascular disease; immune system; neurological; growth; development; cell proliferation; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; ss; gene;
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; 2002US-0413910P.
; 2002US-0414296P.
; 2002US-0417821P.
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Becha SD, Emerling BM, Jin P, Wilson AD,
Chang H, Yang YG, Lee SY, Khare R, Elli
Chawla NK, Ramkumar J, Gururajan R, Tribo
Murage J;
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DB; ADK71829.
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Elliott VS, H
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llliott VS, Hafalia AJA;
ribouley CM, Chien D,
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New human kinases and phosphatases, useful for diagnosing, treating preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, car hepatitis.

Claim 5; SEQ ID NO 65; 347pp; English.

The invention relates to a novel isolated polypeptide which is a human CC kinase and phosphatase (KPP). The polypeptide of the invention CC demonstrates cardiovascular, antiarteriosclerotic, hypotensive, CC vasotropic, antialfammatory, antianginal, anti-HTV, antiallargic, CC antidiabetic, immunosuppressive, antityproid, dermatological, accompathic, antiartritic, uropathic, ophthalmological, antirheumatic, CC antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic, CC antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic, CC haemostatic, cytostatic, antilipaemic, antiparasitic, antihelmintic, CC antibacterial, virucide, protozoacide and fungicide activities. The CC kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and CC disorders such as cardiovascular diseases, immune system disorders, CC neurological disorders, disorders affecting growth and development, cell protozoan or helminthic infections. Furthermore, the molecules of the invention may be useful for creating transgenic animals to model human CC disease and during gene therapy. The current sequence is that of a human CC KPP CDNA of the invention.

Sequence 2599 BP; 541 A; 786 C; 828 ç, 444 T; 0 U; 0 Other;

97.8**%**; 98.3**%**;

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12; Length Indels

35;

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Best Local Similarity
Matches 2253; Conserv 395 301 335 181 215 455 361 241 275 121 155 61 95 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAGTGGATGGCCCAGCGGGTCAAGAGT CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT ATGGGCTTCTTCCGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG ATGGGCTTCTCTGTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAAGGACATTGAGAAGCTGAAGAGC AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG **AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG** GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGAGGATCTGAACTCAGGGCCCCCTGAGC GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGGGATCTGAACTCAGGGCCCCTGAGC Conservative Score 2206.2; Pred. No. 0; 0; Mismatches <u>.</u> ω --480 514 454 360 394 300 334 180 214 120 154 6

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                                                            ATGAGCCTGGGCAGCCCAGCTTCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAA 2245
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AAS95001

D AAS95001 standard; DNA; 2889 BP.

X

C AAS95001;

X

14-FEB-2002 (first entry)

X

WHUMAN DNA sequence #256 expressed during foam cell differentiation.

X

WHUMAN; foam cell differentiation; atherosclerosis; cerebral stroke;

W cardiovascular disorder; coronary artery disease; gene therapy; ds.

X

W Homo sapiens.

X

WO200177389-A2.
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Query Match
Best Local Similarity
Matches 2255; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used PCR primers and probes. The polynucleotide sequences can also be used profession of the invention are also polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation
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human; kinase and phosphatase protein; KPP; enzyme; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
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δ 밁 8

Query Match Best Local S Matches 2078

Similarity

74.1%;

Score 1671.6; DB 13; Pred. No. 1.1e-305; Mismatches

Conservative

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4.

Indels 384; Gaps

ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG

GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCAGCGGGTCAAGAGT ATGGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG

120 154 60 2 Sequence

2623

B₽;

541 A;

786 C;

840 G;

456 T; 0 U;

0 Other Length 2623

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The present sequence encodes the human kinase and phosphatase protein (KPP), designated KPP-43. The human KPP sequences from the present CC invention have cytostatic, antiarreriosclerotic, anticonvulsant, compounds, neuroprotective, carebroprotective, anti-HIV, antiallergic, antiinflammatory and thyromimetic activities, and can be used in gene CC therapy. The human KPP proteins and polymucleotides can be used in GC diagnosing, treating and preventing diseases or conditions associated CC with the decreased expression or overexpression of KPP, such as cell CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g. RIDS, CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. RIDS, CC disorders, or infections. They can also be used in assessing the effects CC of exogenous compounds on the expression of nucleic acid and amino acid CC sequences of KPP. The KPP or its fragments are useful in screening CC compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; gene therapy; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epileps; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; developmental disorder; Hypothyroidism; Cushing's syndrome; infection; KPP-43; single nucleotide polymorphism; SNP; gene; ss.
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19-MAR-2003; 2003US-0456932P
28-MAR-2003; 2003US-0458844P
09-APR-2003; 2003US-0461678P
17-APR-2003; 2003US-0463937P
                                                                                                                                                                                                                                                                                                                                                                                                                                   New human kinases and phosphatases (KPP) for diagnosing, treating and preventing diseases or conditions associated with aberrant KPP expression e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ramkumar J, Marquis JP, Swarnakar A, Chawla NK, Tran U
Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R,
Jackson AA, Yang J, Gorvad AE;
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P-PSDB; ADR39770.
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Qy 2011 AGCGACGTGTGGAGCTTTGGCATCTTGCTCTGGGAGACCTTCAGCCTGGGGGCCTCCCCC 2070	Qy 1951 CAAGTCCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAA 2010		CACCGGGACCTGGCTGCGCGAACTGCCTGGTGACAGAAGAAGAATGTCCTGAAGATCAGT 1	Qy 1771 CTGCAGATGGTGGGGGATGCAGCTGCTGCATGCATGCATG	Qy 1711 GGGGCGACTTCCTGACCTTCCTCGCACGGAGGGGCCCCGCCTGCGGGTGAAGACTCTG 1770	Qy 1651 CGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAG 1710	Qy 1591 AAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTG 1650	Qy 1531 CGAGCCGACAACACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTC 1590	Qy 1471 CTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTTGGCGAAGTGTTCAGCGGACGCCTG 1530	Qy 1411 AGTGGTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGAC 1470	Qy 1351 CCTAGCATTCCTTTGCTCATCGACCACCTACTGAGCAGCCAGC	QY 1321		TACCACGGGGCCATCCCGAGGGCAGAGGTGGCTGAGCTGCTGGTGCACTCTGGGGACTTC		1181 ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTCG	Oy 1201 CTCCTGCAGGATGACCGCCACTCCTCCCAGGTCCTCCGCGCAGGCAG	1061 CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCCCCGCCTGTGCTG

음 성 음

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Query Match
Best Local Similarity
                                                                                                                   The invention relates to a method for inducing neutralisation of cells or tissues by using a protein binding to CRAM (collapsing-response mediator protein-associated molecule) protein or its encoded gene. The proteins and their encoded genes are useful in gene therapy and regenerative medicine, e.g. by inducing neutralisation of mitochondria. They are also applicable in diagnosis, drug development for neural diseases and studying the mechanism of pathosis. The current sequence represents CRAM protein related cDNA.
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27-JAN-1991
The fur gene, encoding furin, is in the human and cat genomes directly upstream of this fes/fps proto-oncogene sequence. Furin is strongly expressed in specific types of tumours and labelled RNA or DNA probes of the fur gene and antibodies against furin can be used for diagnostic purposes. (See also AAN70061-62 and AAP70056). (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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Best Local Similarity
Matches 635; Conserv
                                                                                                                                                                                       Osteopathic; antiinflammatory; antirheumatic; antiarthritic; gene therapy; type II collagen; expression; cartilage diseas
                                                                                                                                                                                                                                                              Gene encoding type II collagen expression promoting protein,
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                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                  ype II collagen; expression; cartilage disease;
cartilage defect; rheumatoid arthritis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
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100.0%; Pred. No. 2.8e-110;
tive 0; Mismatches 0;
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Best Local Sim:
Matches 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a purified protein (I) that promotes type II collagen expression. Also disclosed is an isolated polynucleotide encoding (I), a recombinant vector comprising the polynucleotide and a gene therapeutic agent comprising the recombinant vector as an active ingredient. The proteins, genes, agents and methods are useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid archirits. The current sequence represents a human gene of the invention encoding a protein that promu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New purified protein that promotes type II collagen expression, useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis.
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19-APR-2002; 2002US-0373594P
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ACTGCCTGGTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTTGGGATGTCCCGAGAGG
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                                                          CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA
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Pred. No. 3.4e-61;
0; Mismatches 320;
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This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine nucleic acid sequences of the invention may be useful for drug screening and toxicity assays. The invention is therefore useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines
                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of compound, pharmaceutical agent or environmental pollutant on a cell
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PFIZER PROD INC.
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Best Local
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                                                                                                           GTCCTGATGCCGTGTTCAGGCTCATGGAGCAGTGCTGGGCCTATGAGCCTGGGCAGCGGC
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RESULT 11
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C ADL71054;
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DT 20-MAY-2004 (first entry)
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DE Gene encoding type II collagen expression promoting protein, some encoding type II collagen; expression; cartilage disease; xx

DE Gene encoding type II collagen; expression; cartilage disease; xx

DE Gene encoding type II collagen; expression; cartilage disease; xx

DE Gene encoding type II collagen; expression; cartilage disease; xx

DE Gene encoding type II collagen; expression; cartilage disease; xx

NW Osteopathic; antiinflammatory; antirheumatoid arthritis; human; xx

NN Osteopathic; cartilage defect; rheumatoid arthritis; human; xx

NN Osteopathic; cartilage defect; rheumatoid arthritis; human; xx

NN Osteopathic; antiinflammatory; antirheumatoid arthritis; human; xx
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Best Local Similarity
Matches 573; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New purified protein that promotes type II collagen expression, useful for preventing and treating a cartilage disease, e.g. osteoarthritis, cartilage defect, or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2584 BP;
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19-APR-2002;
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DB; ADL71055.
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                            GGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGC
                                                                                                                     CAGCCTGTCTACATCATTATGGAACTGGTTTCAGGAGGTGATTTCCTCACCTTTCTGAGA
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                                                           AGGAAGAAGGATGAACTAAAACTCAAACAGTTAGTGAAATTTTTCATTAGACGCTGCTGCT
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38043 cDNA sequences, appearing as determined by the technique of SBH included is a purified polypeptide

Claim

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SEQ

ID NO 1503;

44pp; English.

The invention relates to an isolated polynucleotide comprising any or 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence determined by the technique of SBH (sequencing by hybridisation). Alt

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Bs; protein kinase; mine16676human s1; cytostatic; antianginal; hypotensive; cardiant; cardiovascular disorder; heart failure; hypotension; atrial fibrillation; dilated cardiomyopathy; idiopathic cardiomyopathy; angina; prollierative disorder; cancer; melanoma; prostate cancer; cervical cancer; breast cancer; colon sarco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                             9908-00387212
                                                                                                                                                          9908-00387212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.5%;
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Sequence 361 BP; 71

A; 101 C; 120 G; 68 T;

0 U; 1 Other;

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The invention relates to identifying a compound which binds to a Kinase (c) (encoded by a nucleotide sequence of 1868, 403, 545, 361, 473, 3001, 526, 663 or 1448 base pair (bp) as given in the specification) comprising contexting the kinase with a test compound under suitable conditions for binding, and detecting binding of the compound to the Kinase. The method cis useful for identifying a compound which binds to the kinase and also correctly compounds which modify the activity of the kinase. The context is contained by aberrant kinase activity where the disorder includes condition characterised by a deregulation, e.g. an upregulation or a condition characterised by a deregulation, e.g. an upregulation or a condition characterised by a deregulation, e.g. an upregulation or a condition characterised by a deregulation, e.g. an upregulation or a condition characterised by a deregulation, e.g. an upregulation or a condition of cellular growth, Cellular growth deregulation of cellular growth, cellular growth deregulation of cellular continues and context of differentiation and/or cellular hypertrophy, cardiovascular disorders such as heart failure, hypertension, atrial fibrillation, dilated coardiomyopathy, diapathic cardiomyopathy, or anginal, proliferative context such as cancer (including melanoma, prostate cancer, cervical, breast, colon sarcoma). The kinases and antibodies raised against them care useful in one or more method such as screening assays, predictive medicine and methods of treatment. The nucleic acid molecules are useful corrections, to detect kinase and phosphatase mRNA or a genetic conservation, can be conserved and conservation in a kinase and phosphatase gene and to modulate kinase and conservations and conservations. The present sequence is a cDNA for a human protein conservation in a kinase and phosphatase gene and to modulate kinase and conservations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying compound which binds to a Kinase, useful for treating diseases e.g. cancer, by contacting kinase with test compound and detecting its binding to the kinase.
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RESULT 14
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Matches 333
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                                                                                                    GGAAGCC---GATGGGGTCTATGCAGCCTCAGGGGGGCCTCAG 1949
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                                                                                                                                                                                 CTGCTGGCATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGA 1852
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                       standard;
                                                                                                                         ACTGCCTGGTGACAGAAGAATGTCCTGAAGAATCAGTGACTTTGGGGATGTCCCGAGA
                                                                                                                                                                     TCCGCACGGAGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAG
                                                                                                                                                                                                                                                              GGAAGCCCGATTGGGGGTCTATGCAGCCTCAGGGGGGCCTCAG
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                       cDNA; 361
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                        ВP
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Pred. No. 1.9
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15-JAN-2004 (first entry)

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RESULT 15
ABX14976
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Best Local Sim
Matches 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for detecting the presence kinases or phosphatases encoded by nucleotides. The kinases and phosphatases and their encoding nucleic acids are potentially useful drug targets. The present invention may also be useful in diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-1999; 99US-00387212
07-SEP-2001; 2001US-00948802
13-MAR-2003
                         ABX14976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 361 BP; 71 A; 101 C; 120 G; 68 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting and modulating the activity of specified kinases phosphatases which are potentially useful as drug targets.
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                                                ABX14976 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                    AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGCGACTTCCTTGCC
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                                                                                                                                      GGAAGCC---GATGGGGTCTATGCAGCCTCAGGGGGGCCTCAG 1949
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                                                                                                                                                                                       ACTGCCTGGTGACAGAGAAGAATGTCCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1910
                                                                                                                                                                                                                                                                TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAG
                                                                                                                                                                                                                                                                                  CNAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is human protein kinase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
 (first entry)
                                                CDNA;
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Pred. No. 1.9e-46;
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Human; ss; protein kinase; minel6676human sl; cancer; cytostatic; antianginal; hypotensive; cardiant. proliferative disorder; cellular growth related disorder; cardiovascular disorder; heart failure; hypertension; atrial fibrillation; dilated cardiomyopathy;
                                                                                                                                                                                                                                                                        Human protein kinase cDNA mine16676human_s1.
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Homo sapiens.

idiopathic cardiomyopathy; angina.

US6465232-B1 15-OCT-2002

07-SEP-2001; 2001US-00948802.

31-AUG-1999; 99US-00387212

(MILL-) MILLENNIUM PHARM INC

2003-147067/14.

Novel human kinase and phosphatase nucleic acid molecules useful treating cellular proliferative disorders such as cancer, cardiov diseases, hypertension, heart failure and angina. cardiovascular

Claim 7; Fig 5; 47pp; English.

The invention relates to an isolated human kinase and phosphatase nucleic CC acid molecule appearing as ABX14972, ABX14973, ABX14976, ABX14976, and CC ABX14978-ABX14981, or their complement. Also included are: (1) an CC isolated nucleic acid molecule which is at least 90 % identical to the CC nucleotide sequence ABX14973 or ABX14975, or 95 % identical to the CC nucleotide sequence ABX14973 or ABX14975, or 95 % identical to the CC complement, where the nucleic acid molecule encodes a polypeptide having CC a kinase activity; (2) An isolated nucleic acid molecule which hybridises CC to ABX14973, ABX14976, and ABX14978 in 6X saline sodium citrate (SSC) at 45 plusoC, followed by one or more washes in 0.2X SSC, 0.1% CC sodium dodecyl sulphate (SDS) at 65 plusoC, where the molecule encodes a CC polypeptide with kinase activity; (3) a vector comprising the CC polynucleotides, operatively linked to a recombinant regulatory sequence; and (4) expressing a polypeptide by culturing a host cell comprising the CC composition of the nucleic acids are useful as modulating agents in regulating a variety of cellular processes, and fragments are useful as primers or CC hybridisation probes for detecting kinase and phosphatase encoding cardiovascular disorders such as cancer and cellular growth related disorders including cardiovascular disorders such as heart failure, hypertension, atrial CC campina. The present sequence is one of the human kinase or phosphatase cDNAs of the invention

Sequence 361 BP; 71 A; 101 C; 120 G; 68 T; 0 U; 1 Other;

á 밁 Ş 밁 S Query Match
Best Local Similarity
Matches 333; Conserv 80 20 AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGCGACTTCCTGACCTTCC CGAGGATCCTGAAGCAGTACAGCCCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC TCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG 1792 CNAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCC Conservative 13.18; 97.48; 0 Score 296.2; DB 10; Pred. No. 1.9e-46; Mismatches 4. Indels Length <u>ა</u> Gaps 1732 1672 139 79 ü

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Result
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Listing first 45 summaries
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1: 9b ba:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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X12616 Mouse c-fes
M14930 Fujinami sa
J02194 Fujinami sa
AF033810 Fujinami sa
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8.8	8.8	8 8		9.4	9.4	10.0	10.0	10.0	10.1	10.1	10.2				12.0		12.2	13.1	13.1	14.1	14.6		16.6	16.6	16.7
3370	3370	2955	2398	4160	4160	156889	142201	12263	15297	15297	2597	3297	2303	4972	3369	3198	2786	361	361	3882	2950	2947	1171	2069	2994
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AR559315	CQ776660	AX481387	HSRTKEPH	E01406	A06936	AC004586	AC124248	HSFESFPS	AR456324	AR183262	CQ726604	DMFPS85D	DMU50450	BT003462	CQ591168	CQ597087	AB006567	AR236724	AR175607	SRFESTK	HUMTKFER	AF187884	RNFLK	MUSFERT	MMU76762
AR559315 Sequence	CQ776660 Sequence	AX481387 Sequence	Z27409 H.sapiens m	E01406 DNA sequenc	A06936 H.sapiens f	AC004586 Homo sapi	AC124248 Homo sapi	X06292 Human c-fes	AR456324 Sequence	AR183262 Sequence	CQ726604 Sequence	X52844 Drosophila	U50450 Drosophila	BT003462 Drosophil	CQS91168 Sequence	CQ597087 Sequence	AB006567 Ephydatia	AR236724 Sequence	AR175607 Sequence	Y17051 Sycon rapha	J03358 Human tyros	AF187884 Canis fam	X13412 Rat mRNA fo	M32054 Mouse tyros	U76762 Mus musculu

ALIGNMENTS

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Qy 241	Db 252	Оу 181	Db 192	0у 121	Db 132	Q	₽	Ş	Query Match Best Local Matches 225	ORIGIN	000	FEATURES	JOURNAL	TITLE	AUTHORS	REFERENCE	ORGANISM	SOURCE	VERSION	DEFINITION	LOCUS	RESULT 1
1 GAGGGCCTGAGCCGCTTGCTGCGGCAGCACGCAGGAGGATCTGAACTCAGGGCCCCTGAGC 300		1 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT 240		1 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC 180	2 GAGGCCGAGCTTCGTCTACTGGAGGGCCATGAGAAGTGGATGGCCCAGCGGGTCAAGAGT 191	61 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGA	72 ATGGCTTCTCTGAGCTGTGCAGCCCCCAGGGGCCACGGGGTCCTGCAGCAAATGCAG 131	1 ATGGGCTTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60	/ Match 100.0%; Score 2256; DB 6; Length 2674; Local Similarity 100.0%; Pred. No. 0; 1es 2256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		/organism="unknown" /organism="unknown" /mol_type="unassigned DNA"	Location/Qualiflers	human kinase proteins, and uses thereof Patent: US 6340584-A 1 22-JAN-2002;	proteins, nu	;	Unclassified. 1 (bases 1 to 2674)	Unknown.	Unknown.	AR183261.1 GI:20226854	1 from patent US 634	AR183261 2674 bp DNA linear PAT 20-APR-2002	

1201 CTCCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGCAGGAGGGGGGAAGG 1260	
RESULT 2 AR456323 AR456323 LOCUS DEFINITION Sequence 1 from patent US 6686187. ACCESSION AR456323 VERSION AR456323 VERSION AR456323 SOURCE Unknown. ORGANISM Unclassified.	1392 AACCTGTACCAACTGGAAAGGGTTTCCTAGCATTCCTAGCACTCCCAACACCTA 1451

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Db 852 TACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGCTGCCACCCTGTGTCACGTTC OY 841 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCCAGCTGAACGAG	Db 792 GTGGTGGCCATTCCTGCGACAGGTATGGGTCCGCACCTGACGCTGCACGCTTC Oy 781 TACCAAGGCTTCCTGCGACAGGTATGGGGTCCGCACCTGACGCTGCACGCTTCACGCTTCCACGTTCCACGTTCCACGTTCCACGTTCCACGTTCCACGTTCCACGTTCCACGTTCCACGTTTCACGGTACGGTATGGGTCCGCACCTGACGTTCCACGTTTCACGTTCCACGTTTCACGTTCCACGTTTCACGTTCCACGTTTCACGTTCCACGTTTCACGTTCCACGTTTCACGTTCCACGTTTCACGTTTCACGTTCACGTTTCACGTTCACGTTTCACGTTCACGTTTCACGTTCACGTTTCACGTTCACGTTTCACGTTCACGTTCACGTTCACGTTCACGTTCACGTTCACGTTTCACGTTTCACGTTTCACGTTTCACGTTCACGTTCACGTTCACGTTCACGTTCACGTTTCACGTTTCACGTTCACGTTCACGTTTCACGTTCACGTTTCACGTTTCACGTTCACGTTCACGTTCACGTTCACGTTCACGTTCACGTTTCACGTTTCACGTTACACGTTCACGTTCACGTTCACGTTCACGTTCACGTTTCACGTTACACGTTTCACGTTCACGTTCACGTTCACGTTCACGTTCACGTTTCACGTTCACGTTCACGTTCACGTTTCACGTTCACGTTCACGTTTCACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACGTTACACACGTTACACACGTTACACACGTTACACACAC	661 732	Oy 601 CACCAGCTCCTGCTGCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGCT	QY 541 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCACCACCACCACCACCACCACCACCACCACCACC		Qy 421 CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCCAAGCGCAAGTACCAGGAGGCCAGC	QY 361 CAGCAGCTGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCCTGAAGAGC	OY 301 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGAGCCTACAGCGAGCAGTGG	Qy 241 GAGGGCCTGAGCCGCTTGCTGCGGCAGCAGAGAGATCTGAACTCAGGGCCCCTGAGC	QY 181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCAGTCCTGGGCTGAGATCACCAGCCAAACT	QY 121 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC	Qy 61 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAGTGGATGGCCCAGCGGGTCAAGAGT	GGGCTTCTCTGAGCTGTGCAGCCCCCAGGGCCACGGGTCCTGCAGCAA! 	Query Match 100.0%; Score 2256; DB 6; Length 2674; Best Local Similarity 100.0%; Pred. No. 0; Matches 2256; Conservative 0; Mismatches 0; Indels 0; Gaps	rce	TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof JOURNAL Patent: US 6686187-A 1 03-FEB-2004; FEATURES Location/Qualifiers	RS CE
911 Oy 900 Db	00 Db 851 Oy 840		660 Db 731 Ov	600 Db 671	540 Qy 511 Db	480 Qy 551 Db	420 CF Db 491	360 Oy 431 Db	300 Oy 371 Db	240 Db	180 Db .	120 Oy 191 Db	60 Qy 131 Db	0; 0b Qy	5 B &	QY	מם
1932 GIGACAGAAGAAIGICCIGAAGAICAGICAGITIGGGAIGICCGGAGAGAAGCCGAI 1991 1921 GGGGTCTATGCAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCGCACCTGAG 1980	72 ATGGAGTACCTGGAGAGCAAGTGCTGCATCCACCGGGACCTGGCTGCTCGGAACTGCCTG 51 GTGACAGAGAAGAATGTCCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGAT		1811 CCCATCTACATCGTCATGGAGCTTGTCAGGGGGGGGGGG	CTGAAGCAGTACAGCCACCCAACATTGGTGCGTCTCATTGGTGTGTCTGCACCCAGAAGCAG 	61 TCTTGTCGAGAGACGCTCCCACCTGACCTCAAGGCCAAGTTTCTACAGGAGCGAGGATC	1501 AACTTTGGCGAAGTGTTCAGCGGACGCCTGCCGAGCCGA	12 AAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTGGGTGAGCAGATTGGACGGGGG	, 2 +	ACCTGTACCGACTGGAAGGGAAAGGCTTTCCTAGCATTCCTTTGCTCATCGACCACCTA	ACACCCAGGCIGGAGAICCTTAAGAGCCACAICTCAGGAATCTICCGCCCCAAGGICTCCGC	TreetigeAggartgAccgccActrcCAcgtcGricctCGGAGCAGGAGGGGGGAGGGGGGAAGG	1 CAGAGTTGCTGCAGACCAAGCTGAAGCACTGGGCCCCGGGGAGCCCCCGCCTGTGCTG	1 CAAGAACCACTGCAGGGGCTGCAGGTAGCCCTGCAGCCCAAGCTGCAGGCCCAG 	I GAAGAGAGAACACCCACCCCGGGAGGGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCTG	1 ACCGACATGGTGTTCAGGCGGCAGGAGATGGTTAGGCAGCTGCAGCAGGAGCTCCGGAAT		2 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGGCTGGGGGAGCTCCAGCTGGAGCGAG

Oy 241 GAGGCCTGAGCGCTTGCTGCGGCAGCACGCAGAGAATTCAGGCCCCTGAGC 300	181 CGGGCCATCAGCCCTGACAGCCCCATCAGTCCTGGGCTGAGATCACCAGCCAAACT 2	OY 121 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGCCAGAGC 180	61 GAGGCCGAGCTTCGTCTACTGGAGGCCATGAGAAAGTGGATGACCCAGCGGGTCAAGAGT 1 	1 AIGGGCTICTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG 60	Query Match 90.2%; Score 2036; DB 6; Length 2697; Best Local Similarity 91.5%; Pred. No. 0; Matches 2256; Conservative 0; Mismatches 0; Indels 210; Gaps 1;	dp/ /moj /orç	Patent: WO 0 PE Corporati Loc	AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses	ORGANISM Homo Baptens ORGANISM Homo Baptens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	ION CQ725220 N CQ725220.1 G: DS .	CQ725220 2697 bp	Db 2292 TACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2327	2101 AGGETCATIGGAGCAGTGCTGGGCCTATGAGCCTGGGC 2232 AGGCTCATGGGCAGGCAGTGCTGGGCCTATGAGCCTGGGC	2161 AGGCTCATGAGGAGGAGGGGGCCCTATGAGCGGGAGCGGCCCAGAGCTTACAGAGCGATGCCAGAGGCGGGGGGGG	2112 TGGGAGACCTTCAGCCGGGGCCTCCCCCTATCCCAACCTCTCAGCAATCAGCAGACACGG	a n—r	1081
9 Y B	성 B &	\$ \$ \$	B &	₽ Q	g 4g	B &	g &	g &	₽ &	Db Qy	D Qy	в Q	B 8	₽ Q	B &	유	Db
1331 CTCCCTCCACCGCTGCAGCTCATTCCGGAGGTGCAGAAGCCCCTGCATGAGCAGCTGTGG 1390 1321 1320 1391 TACCACGGGGCCATCCCGAGGGCAGAGGTGGCTGAGCTGCTGGTGCACTCTGGGGACTTC 1450	ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCCAAGTTCTCG	1201 CTCCTGCAGGATGACCGCCACTCCACGTCCTCCGGAGCAGGAGCGAGGAGGGGGGAAGG 1260		1081 CAAGAAGCACTGCAGGGGCTGCAGGTAGCCCTGTGCAGCCAGGCCCAAGCTGCAGGCCCAG 1140		961 ACCGAGATGGTGTTCAGGCGGCAGGAGATGGTTACGCAGCTGCAACAGGAGCTCCGGAAT 1020	901 CTGACTGTGGAGAGCGTGCAGCACACGCTGACCTCAGTGACAGATGAGCTGGCTG	841 GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGGAGCTCCAGCTGAACGAG 900	781 TACCAAGGCTTCCTGCGACAGTATGGGTCCGCACCTGACGTCCCACCCTGTGTCACGTTC 840	721 GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCTGCTGCCGCATCCAGCCTGAGGCTGAG 780	661 TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGCCTGGTGCAGGATGAG 720	601 CACCAGCTCCTGCTGCCGGCCTGCTGCGGTCACTGCAGGACCTGCACGAGGAGATGGCT 660	541 GCTCACCACAACCGCTATGTGCTGGGCGTGCGGGCTGCGCAGCTACACCACCAGCACCAC 600	481 AAAGACAAGGACCGTGACAAGGACAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT 540	421 CAGTACCGAGCTCTGGCACGGACAGTGCCCAAGCCAAGC	361 CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGGCCAGGACATTGAGAAGCTGAAGAGC 420 	311 AAGCTGAGCCTGCTCATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG 370

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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

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Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

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Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: e Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13376997.
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, &
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
A.N., Gibbs, R.A.
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
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Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens feline sarcoma o IMAGE:5170548), complete cds. BC035357
BC035357
BC035357.1 GI:23271524
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1 (bases 1 to 2788)
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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2771)

Alcalay, M., Antolini, F., Van de Ven, W.J., Lanfrancone, L., Grignani, F. and Pelicci, P.G.

Characterization of human and mouse c-fes cDNA clones and
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Homo sapiens (human)
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CYTPDESLLEEGEPLEFGELQLNELTYVESVQHTLTSVTDELAVATEMVFRRQEMVTQL

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LDNLYRLEGEGFPSIPLIDHLSTQOPLTKKSGVYLLRAVPKDKWYLAHEDLVLGEQ

IGRONFGEVESGRLRADNTLVAVKSCRETLPDLKAKFLQEARILKQYSHPNIVRLIG

VCTQKQPIYIVMELVQGGDFLFFLTETEGARLRVKTLLQMVGDAAAGMEYLESKCCIHR

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/protein_id="CAA36438.1"
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mol_type="mRNA"
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Genes expressed in foam cell differentiation
Patent: WO 0177389-A 256 18-OCT-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wilks, A.F. and Kurban, R.R.
Isolation and structural analysis
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Mouse c-fes proto-oncogene mRNA
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Query Ma Best Loo Matches	Query Match 68.3%; Score 1540.4; DB 10; Length 2680; Best Local Similarity 79.2%; Pred. No. 2.5e-258; Matches 1954; Conservative 0; Mismatches 296; Indels 216; Gaps 2;
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망	120 GAAGCTGAGCGCTTATTGGAGGGCATGAGGAAGTGGATGGCCCAGAGGGGTCAAGAGT 179
Ş	121 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCCCTGCAGGACAGTGGGGGGCCAGAGC 180
뭥	180 GACCGGGAATATGCAGGATTGCTTCACCACATGTCCTTGCAGGACAGCGGAGGCCAGAGC 239
Ş	181 CGGGCCATCAGCCCCTGACAGCCCCATCAGTCCTGGGCTGAGATCACCAGCCAAACT 240
В	240 TGGAGCAGGCCCGGACAGCCCTGTCAGCCAGTCCTGGGCAGAGATAACAAGCCAGACC 299
Ş	241 GAGGGCCTGAGCCGCTTGCTGCGGCAGCAGCAGCAGCATCTGAACTCAGGGCCCCTGAGC 300
Ъ	300 GAGAACTTGAGCCGGGTGCTGCGGCAGCATGCAGAAGATCTGAACTCGGGGCCCTTGAGC 359
8	301 AAGCTGAGCCTGCTCATCCGGGAAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG 360
늉	360 AAACTGAGCGTGCTGATCCCGGAGGCGCACAGCCTGAGAAAGACGTACAACGAGCAGTGG 419
Ş	361 CAGCAGCTGCAGGAGGTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGAGC 420
рb	420 CAGCAGCTGCAGCAGGAGCTCACCAAGACCCACAGCCAGGACATTGAGAAGCTGAAGACT 479
Ş	421 CAGTACCGAGCTCTGGCACGGGACAGTGCCCAAGCCAAG
Db	480 CAGTACCGGACCCTGGTACGAGATAGCACCCAGGCCAGG
γ	481 AAAGACAAGGACCATGACAAGGACCAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTT 540
Db	540 AAAGACAAGGATCGAGACAAGGCCAAAGACAAGTATGTCCGGAGCCTGTGGAAGCTCTTT 599
γ	541 GCTCACCACACCGCTATGTGCTGGGCGTGCGGGCTGCGCACCACCACCACCACCACCACCACCACCACCACCACC
Db	600 deceaecacada de construcción de construcci
Qy	601 CACCAGCTCCTGCCGGCCTGCTGCGCGTCACTGCAGGACCTGCACGAGGAGATGGCT 660
망	660 CACCGGTTCATGCTGCCTGCCTGCAGTCACTGCAGGATTTGCACGAGGAGATGGCG 719
Qy	661 TGCATCCTGAAGGAGATCCTGCAGGAATACCTGGAGATTAGCAGGCTGGTGCAGGATGAG 720
Db	720 GCATTCTGAAGGACATCCTGCAGGAATACCTGGAGATTAGCAGTCTGGTGCAGGACGAT 779
8	721 GTGGTGGCCATTCACCGGGAGATGGCTGCAGCTGCCCGCATCCAGCCTGAGGCTGAG 780
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	1591 AAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCCCCAACATCGTG 1650	음 성
	1531 CGAGCCGACAACACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGACCTC 1590	ል
	1471 CTGGTGTTGGGTGAGCAGATTGGACGGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTG 1530	ъ У
	1411 AGTGGTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGAC 1470	유 성
	351 CCTAGCA	8
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	494 CTGGTTCGGGAGAGCCAGGGCAAGCAGGAGTATGTACTGTCTGT	9
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	314 ACACCACACTGGAGATCCTTAAAAGCCACTTCTCCGGAATCTTCCGCCCCAAGTTCTCT 13	db
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	1201 CTCCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGCAGGAGGCGAGAGGGGGGAAGG 1260	Ş
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	CACCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAC	र्
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	00 GATGAGTCGCTTCTTGAAGACGGGGAACAGCTGGAGCCAGGGGAGCTGCAGCTGAAT	8
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ACFTS140A

Pujinami sarcoma virus temperature sensitive (ts) p140 transforming protein RNA, 3' end.

NM14930

M14930.1 GI:209688

Stransforming protein.

Pujinami sarcoma virus

Pujinami sarcoma virus

Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.

1 (bases 1 to 2715)

Chen,L.H., Hatada,E., Wheatley,W. and Lee,W.H.

Single amino acid substitution, from Glu1025 to Asp, of the fps oncogenic protein causes temperature sensitivity in transformation and kinase activity

ACFTS140A

2715 bp ss-RNA

1 linear VRL 27-APR-1993

M140 transforming protein causes; Retroviridae; Alpharetrovirus.
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                                       Original source text: Fujinami sarcoma pFL-5 from ts FL-15.
                                                                    Virology 155 (1), 106-119 (1986)
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Query Match
Best Local Similarity
Matches 1641; Conserv
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                                                                                                                                                c-myc proto-oncogene; complete genome; fps oncogene; polyprote Pujinami sarcoma virus Pujinami sarcoma virus Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.

1 (bases 1 to 4788)

1 (bases 1 to 4788)

Shibuya, M. and Hanafusa, H.
Nucleotide sequence of Fujinami sarcoma virus: evolutionary relationship of its transforming gene with transforming genes other sarcoma viruses

Cell 30 (3), 787-795 (1982)
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                                                              2 (bases 1832 to 1881; 2851 to 2902)
Carlberg,K., Chamberlin,M.E. and Beemon,K.
The avian sarcoma virus PRCII lacks 1020 nucleotides of the
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The sequence of 1182 amino acids was deduced from the Fujinami sarcoma virus (FSV) transforming protein p130, the product of gag-fps fused gene. p130 is highly homologous to the gag-fes sequence of feline sarcoma virus (see separate entries), and is homologous in the 280 residue carboxyl end (including the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein.
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        CTGGGACATCTCCGTGCCACCGACCACAGCAGCCAGATCGGGGGAGTCGTGGTGGTTCTG 1939
                                                                                                                                                 GACAGGGAGTATGCAGGACTGCTTCACCACATGTCC------CTGCAGGACAGT 168
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                                                       ATGGGCTTCTCTTCTGAGCTGTGCAGCCCCCAGGGCCACGGGGTCCTGCAGCAAATGCAG
                                                                                                                    GACCGGGAGTACGCGGGGATGCTGCACCACATGTTCTCTCAGCTGGAGAAACAGGAGGGC
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SQRAKSDREYAGMLHHMFSQLEKQEGLGHLRAYDHSSQLESSWWYLASQTETLSQTIR
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RDSTQAKKKYQEASKDKEREKAKEKYYRSLSKLYALHNQYVLAYQAALHHHHYQRA
LPTILHESLYSLQQBWYLVLKEILGEYCSITSLYQEDVLAHIQKYAHAVEMIDPATEYS
SFYQCHRYDSEVPPAVTFDESLLEEANLIEGELQLURLTIESVQHSLTSIEEELLAS
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MEYLBSKHCHRDLAARNCLYVEKWTLKISDFGMSGDESDGYYASTGGMKQI DYKWTA
PEALMYGMYSSESDWASFGILLWEAFSLGAVPYANLSNQQTREAIEQGVRLEPPEQCP
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/db_xref="GI:209667"
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/tranlation="MREVIKGELKTWGLVLGALKAAREEQVTSEQAKFWLGLGG
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CATASAPPPFYVGSGLYPSLAGVGEQQQQGGDTPRGAEQPFALEW
ARIRELASTGPPMYAMPVVIKTEGPAPHALMMDAMA.SGQLHR.PQPGEHTSTSAAAGTWRL
ALMSSELLPHDVTNEMEVILGBA.PHALMMDAMA.SGQLHR.PQPGEHTSTSAAAGTWRL
ALMSSELLPHDVTNEMEVILGBA.PHALMMDAMA.SGQLHR.PQPGEHTSTSAAAGTWRL
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/mol_type="genomic RNA"
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229 ACCAGCCAMACTTAGGGCCTGACCCGATTGCTGCCGCCGAGGGATCTTGAACTCA 288 289 GGCCCCTGAGCCACTTGACCCGCTTGACCCCGCAGGGATCTTGAACTCA 288 289 GGCCCCTGAGCCACTTGACCAGGATCGAACGCTGCAACCTTGCAACCTCA 348 200 GGCCCGTGACCAGTTGACCAGGATCGAACGCTGCAACCTTGCAAGCCTAAGCCAAGCCCCAAGCCCAAGCAACACCCAAGCCCAAGCAACACCCAAGCCCCAAGCCCCAAGCCCCAAGCCCCAAGCCCCAAGCCCCAAGCCCCAAGCCCCAAGCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCAAGCCCCCC
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RETROVIRUSES: 757;
Cold Spring "
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AF033810
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Submitted (12-NOV-1997) NIH,
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Appendix 2: Retroviral taxonomy,
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Viruses; Retroid viruses;
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AQRDMLANKLAELGSEBPPALPLQEDBGSARSTDQERSGVTALKTIKNHISGIFSPR
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MEYLESKHCIHRDLAARNCLVTEKNTLKISDFGMSRQEEDGVYASTGGMKQIPVKMTA
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WDGQPRHFIIQAADNLYRLEDDGLPTIPLLIDHLLQSQRPITRKSGIVLTRAVLKDKW
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                                                                                     /product="p14 MA"
899. .1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Fujinami sarcoma virus"
/mol_type="genomic RNA"
/db_xref_"taxon:11885"
                 /product="CA"
1307. .3925
                                                                                                                                        EDVYRLMQRCWEYDPHRRPSFGAVHQDLIAIRKRHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="p140 polyprotein"
/protein_id="AAC82565.1"
/db_xref="GI:2801467"
   product="FBS"
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1085. .1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="p140 polyprotein"
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1 (bases 1 to 4901)

1 (bases 1 to 4901)

Van Groningen, J.J., Van den Ouweland, A.M., Verbeek, J.S., Vemp, A.W., Bloemers, H.P. and Van de Ven, W.J.

Structural analysis of a variant clone of Snyder-Theilen
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Figure 4. Nucleotide sequence
clone of ST-FeSV.
M22820
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                                          CAGACCAAGCTGGAGCACCTGGGGCCCGGCGGGGCGCCGCCTGTGCTGCTCCTGCAGGAT
                                                                              CAGGCGCTGCAGGTGGCGTTGTGCAGCCAGGCCAAGCTGCAGGCCCAGCGGGAGCTGCTG
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/mol_type="unassigned DNA"
/db_xref="taxon:12908"
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mat_peptide	2083 AGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGGCCGTCTGCCCTGCCCAGAGCTG 2142	ફ
mat_peptide	3074 AGCTTCGGCATCTTGCTATGGGAGACCTTCAGCCTGGGGGCCTCCCCCTATCCCAACCTC 2082	B 6
	AAGTGGACGGCACCCGAGGCTCTTAACTACGGCCGCTATTCCTCTGAGAGCGACGTGTGG) B
	1963 AAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTCCGAAAGCGACGTGTGG 2022	ई
	1903 TCCCGAGAGGAAGCCGATGGGGTCTATGCAGCCTCAGGGGGCCTCAGACAACTCCCCGTG 1962	B &
	GCTGCTCGGAACTGCCTGGTGACGGAGAAGAACGTCCTGAAGATCAGTGACTTCGGGATG	망
	1843 GCTGCTCGGAACTGCCTGGTGACAGAGAAGAATGTCCCTGAAGATCAGTGACTTTGGGATG 1902	ş
	1783 GGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGTGCTGCATCCACCGGGACCTG 1842	B 8
	2774 CTGACCTTCCTGAGGACGGAGGGAGCCCGCCTGCGGATGAAGACGCTGCTGCAGATGGTG 2833	Вþ
CDS	1723 CTGACCTTCCGCACGGAGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTG 1782	Ş
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	GTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGG	Ş.
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tor pr	ACTOTAGE USECCE TRANSPORT TO SECOND COORDINATE TO S	? 5
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garcom with t	1483 GAGCAGATTGGACGGGGAACTTTGGCGAAGTGTTCAGCGGACGCCTGCGAGCCGACAAC 1542	ş
	2474 CTCAACAGGCTGTGCCCAAGGACAAGTGGGTGCTAAACCACGAGGACCTGGTGTTGGGT 2533	90
MEDLINE 830509	1423 CTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAGGACCTGGTGTTGGGT 1482	8
Ham Nuc evi	1363 TTGCTCATCGACCACCTACTGAGCACCCAGCAGCCCCTCACCAAGAAGAGGTGGTGTTGTC 1422	g &
	2354 ATCATCCAGTCCGCTGACAACCTCTACCGACTGGAAGGAA	Вb
ORGANISM Feline	1321AACCTGTACCGACTGGAAGGGGAAGGCTTTCCTAGCATTCCT 1362	ş
DS 2	2294 AGCCAGGGCAGGAATATGTGCTGTCGGTGCTGTGGGACGGCCAGCCCCGCCACTTC 2353	ф
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-	2234 CTCCCACGGCCAGAGGTGGCTGAGCTGTTGACGCACTCTGGGGACTTTCTGGTGCGCGAG 2293	ఠ
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2143	GAGATCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTCG	ş
3134	2054 GACCGCCACTCCACGTCGTCCTCGGAGCAGGAGCGAGAAGGGAAGGACACCCACC	В

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bases 1 to 2397)

e.A., Laprevotte,I., Galibert,F., Fedele,L.A. and Sherr,C.J. eotide sequences of feline retroviral oncogenes (v-fes) provide ence for a family of tyrosine-specific protein kinase genes 30 (3), 775-785 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transforming polyprotein of the snyder-theilen strain of feline oma virus (feev) include the transforming gene (fee) product tyrosine specific protein kinase activity, the encoded protein ence was compared with the gene products of gardner-arnstein strain (see fesyganc), fps gene of avian fujinami sarcoma streain (see feryganc), fps gene of avian fujinami sarcoma se (see fsv), and src gene of avian sarcoma virus, the reported ence contains a 145bp deletion against the ga strain, and the ors argue that they sequenced a defective clone, the missing entides are denoted by n's (see fevgaonc between 1818 and 1964 presumed base sequence), the last 24 bases represent the ence of feline leukemia virus.
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                                                                                                                                                                                                  proto-oncogene;
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/product="protein p30"
892. .2256
                                                                                                                                                                                  VFRLMEQCWAYEPGQRPSFSAFYQELQSIRKRHR"
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/product="gag_polyprotein"
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/db_xref="GI:7548235"
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/db_xref="taxon:11772"
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/mol_type="genomic RNA"
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                                                                         product="protein
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'product="v-fes transforming protein"

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feline 88
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Hampe, A., Laprevotte, I., Galibert, F., Fedele, L.A. and Sherr, C.J.
Nucleotide sequences of feline retroviral oncogenes (v-fes) provide
evidence for a family of tyrosine-specific protein kinase genes
Cell 30 (3), 775-785 (1982)
                                                                                                                                                                                                                                    the transforming polyprotein of the gardner-arnstein strain of feline sarcoma virus (fesv) include the transforming gene (fes) product with tyrosine specific protein kinase activity. The encody protein sequence was compared with the gene products of snyder-theilen strain (see fesvetonc), fps gene of avian fujinami sarcoma virus (see fsv), and src gene of avian sarcoma virus. the last 24 bases represent the sequence of feline leukemia virus. Location/Qualifiers
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/db_xref="GI:332873"
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                                                                                                                                              /organism="Gardner-Arnstein
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/db_xref="taxon:11824"
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YQBASKDKDRDKAKLBQLGFGBPPVLLLQDDRHSTSSSEQBREGGRTPTLBILKSHI
SGIFREKFSLPPPLQLVPEVQKPLHEQLWYHGALPARENGARPTLHSGDELVRESQGKQ
EYVLSVLWDGQPRHFIIQSADNLYRPBGDGFASIPLLVDHLLBSQQPLTKKSGIVLNR
AVPKDKWVLNHEDLVLGEQIGRGNFGEVFSGRLRADNTLVAVKSCRETLPPDIKAKFL
QBAKILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDPTHFLRTEGARLRMKTILQM
VGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFMSREAADGIYAASGGLRQ
VVKWTAPEALMYGRYSSESDVWSFGILLWETTSLGASPYPNLSNQQTREFVEKGGRL
PCPELCPDAVFRLMEQCWAYEPGQRPSFSAIYQELQSIRKRHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="protein 592. .1044
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QVKQVVQGKEETPAAARADGTMGFSSELCSPQGHGAEQQMQEAELRLLEGMRKMMAQR
VKSDREYAGLLHHMSLQDGGGRGTGPYSPISQSWAEITSQTEGLSRLLRQHAEDLNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="protein p15"
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Pred. No. 2.8e-131;
0; Mismatches 182;
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                                                           CE 2 (bases 1 to 4788)

CE 2 (bases 1 to 4788)

Strausborg, R. L., Feingold, E. A., Grouse, L. H., Derge, J.G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Banaldo, M. F., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,

Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,

Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Mullahy, S. J., Bosak, S. A., McBwan, P. J.,

McKernan, K. J., Malek, J. A., Gunarattne, P. H., Richards, S.,

Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,

Bouffard, G. G., Blakesley, R. W., Touchman, W., Green, E. D.,

Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,

Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,

Schnerch, A., Schein, J. E., Jones, S. C. and Marza, M. A.

Generation and initial analysis of more than 15.000 full-length
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1 (bases 1 to 4788)
Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W.
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Xenopus laevis MGC80946 protein, IMAGE:5516233), complete cds.
                  Generation and initial analysis of more than 15,000 human and mouse cDNA sequences
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Feathbrastone, Malachi Griffith, Obi Griffith, Ran Guin, Wancy Liao Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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Submitted (14-JUN-2004) National Institutes of Health, Xenopus Gene Submitted (XGC), National Institute of Child Health and Human Collection (XGC), National Institute of Child Health, MD
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
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20892-7510, USA
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KQLHSD I A I EEKTTDCREQLNILLAKRHALRDALLQYHMTLCNKNK I QGQREMLKROM
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DLWASFGILLWENY JENSTANDHONG PROTINGAT LGGGRAFGEVESKHCI HR
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                    Score 656.4; DB 5;
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194	888
C 1887	1828 ATCCACCGGGACCTGGCTGGCTCGGAACTGCCTGGTGACAGAAGAAGAATGTCCTGAAGATC
IC 1827	1768 CTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCATGGAGGAGCCAAGTGCTGC
T 1767 G 2375	1708 CAGGGGGCGACTTCCTGACCTTCCTCCGCACGGAGGGGGGCCCGCCTGCGGGTGAAGACT
G 1707 G 2315	1648 GTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGCCCATCTACATCGTCATGGAGCTTGTG
C 1647	1588 CTCAAGGCCAAGTTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACCCCAACATC
C 1587	1528 CTGCGAGCCGACAACACCCTGGTGGCGGTGAAGTCTTGTCGAGAGACGCTCCCACCTGAC
C 1527 C 2135	1468 GACCTGGTGTGGGTGAGCAGATTGGACGGGGGAACTTTGGCGAAGTGTTCAGCGGACGC
G 1467 A 2075	1408 AAGAGTGGTGTTGTCCTGCACAGGGCTGTGCCCAAGGACAAGTGGGTGCTGAACCATGAG
G 1407 A 2015	1348 TITCCTAGCATTCCTTTGCTCATCGACCACCTACTGAGCACCCAGCAGCACCCACC
C 1347	1320
G 1895	1836 TTCCTTGTCCGGGAGAGCCAGGGCAAGCAAGAATATGTGCTGTCTGT
- 1319	0
-	6 TGGTACCATGGTGCCATACCTCGCTCTGAAGTCCAAGGACTGTTGGTGAATCGAGGGGA
	0
C 1319	1277TCCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCAAGTTCTC
- 1276 T 1715	1249 GAGGGGGAAGGACACCCACGCTGGAGA
A 1248 T 1655	1189 CCGCCTGTGCTGCTGCAGGATGACCGCCACTCCACGTCGTCCTCGGAGCAGGAGCGA
C 1188 T 1595	1129 CTGCAGGCCCAGCAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCCGGCGAGCCC
 G 1535	

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                                                                                   1682 CCATCTACATCGTCATGGAGCTTGTGCAGGGGGGGGGACTTCCTGACCTTCCTCCGCACGG
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synthetic construct
other sequences, artificial sequences.

1 (bases 1 to 856)
1 (bases 1 to 856)
Van de Ven,W.J.M., Roebroek,A.J.M. and Schalken,J.A.
Recombinant DNA, mRNA, protein, antibodies, and a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of detecting tumor cells patent: EP 0246709-A 2 25-NOV-1987; Stichting Katholieke Universiteit Location/Qualifiers
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fes/fps-related mRNA.
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                 AGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGCTGCTGGCA 1801
                                                                                                                                                       TGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGC
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                                                                                                                                   TGAAGCAGTACAGCCACCCCAACATCGTGCGTCTCATTGGTGTCTGCACCCAGAAGCAGC
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AGGGGGCCCGCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGGATGCAGCTGCTGGCA
                                                                   CCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCACGG
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                     /codon_start=1
/trans1 table=11
/product="fee/fps-related protein"
/product="fee/fps-related protein"
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RVKTILQMVGDAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREERDGVY
AASGGLRQVPVKWTAPEALNYGRYSGESDVWSFGILLMETFSLGASPYNLSNQQTRE
FVEKGGRLPCPELCPDAVFRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Protein sequence is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="synthetic construct"
/mol_type="unassigned RNA"
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1802 TGGAGTACCTGGAAGAGCAAGTGCTGCATCCACCGGGACCTGGCTCCGGAACTGCCTGG [181]	Sear	Вb	δ	망	Ş	Вb	₽.	망	\$	용	8	밁	Ş	F	8	DЬ	Ş
	March 19, 2005, 8 secs	601 ACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG	2222 ACCAGGAGCTGCAGAGCATCCGAAAGCGGCATCGG	541	2162	481	2102	421	2042	361	1982	301	1922	241	1862	181	1802
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